

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 20, 2002, 23:30:41 ; Search time 1336.89 Seconds

11439.150 Million cell updates/sec

Title: US-09-530-209A-1
Perforated Score: 037

Sequence: 1 ATGGCAGAGGAATCTAGA.....CTTATACACATCTTCTTAA 927

Scoring table: IDENTITY_NUC

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

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Minimum DB seq length: 0
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Maximum DB seq length: 20000000000

Pre-processing:	Minimum Match	08
Post-processing:	Minimum Match	08

Listing first 45 summaries

Database : GenEmbol

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3:	gb_in.*
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5:	gb_ov.*
6:	gb_pat.*
7:	gb_ph.*
8:	gb_pl.*
9:	gb_dr.*
10:	gd_ro.*
11:	gb_sts.*
12:	gb_sy.*
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15:	em_ba.*
16:	em_fun.*
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18:	em_in.*
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24:	em_pl.*
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26:	em_sts.*
27:	em_sy.*
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34:	em_htg_inv.*
35:	em_htg_rod.*
36:	em_htg_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							
1	927	100.0	927	6	A96985	A96985	Sequence 1
2	927	100.0	1179	8	ATH131636	ATH131636	Arabidopp
3	302.2	32.6	1284	8	MA5057	MA5057	Sequence 1
4	302.2	32.6	1284	8	NTA011892	NTA011892	Nicotlann
5	266	28.7	1650	8	ATCD2	ATCD2	A.thaliana
6	261.2	28.2	88356	8	ABO11479	ABO11479	Arabidopp
7	258.2	27.9	1699*	8	CRCYCD	CRCYCD	C.rubrum m
8	193.4	20.9	1846	6	AB5077	AB5077	Sequence 2
9	148.2	16.0	113053	8	ATF12B17	ATF12B17	Al353995
10	127.8	13.8	1679	6	AB5058	AB5058	Sequence 2
11	127.8	13.8	1679	8	NTA011893	NTA011893	Nicotlann
12	126.2	13.6	1140	8	AMA250397	AMA250397	Antirrhilop
13	126.2	13.6	1414	6	AB5061	AB5061	Sequence 5
14	126	13.6	1487	8	ABO15222	ABO15222	Nicotlann
15	123.2	13.3	1788	6	AB5059	AB5059	Sequence 3
16	118.4	12.8	1431	6	NTA011894	NTA011894	Nicotlann
17	118.4	12.4	1518	8	LEA15588	LEA15588	Lycopers
18	115.4	12.4	1518	8	LEA25415	LEA25415	Lycopers
19	115.4	12.4	1532	8	AMA250366	AMA250366	Antirrhilop
20	111.2	12.0	1162	8	ATCD1	ATCD1	A.thaliana
21	111.2	12.0	1951	8	LEA15589	LEA15589	Lycopers
22	110.6	11.9	1460	8	ABO08188	ABO08188	Pisum sat
23	107	11.5	1628	8	AMA250398	AMA250398	Antirrhilop
24	106.2	11.5	1451	8	MSCYCPROT	MSCYCPROT	M.sativ
25	104.2	11.2	1461	8	LEA15590	LEA15590	Lycopers
26	101	10.9	1449	8	CRU011776	CRU011776	A.thaliana
27	99.8	10.8	1214	8	ATCD3	ATCD3	Sequence 1
28	93	10.0	1632	8	AC006592	AC006592	Arabidopp
29	84.2	9.1	102051	8	ABO25614	ABO25614	Arabidopp
30	76.6	8.3	15290	8	AP003744	AP003744	Oryza. sat
31	64.2	6.9	112512	8	ATF344	ATF344	Arabidopp
32	60.2	6.5	108158	8	MSA12930	MSA12930	Medicago
33	59.8	6.5	3054	8	AXO83744	AXO83744	Medicago
34	59.6	6.4	4553	8	ATF28A23	ATF28A23	Arabidopp
35	57.6	6.2	1141	6	ATCHRIV80	ATCHRIV80	Arabidopp
36	57.6	6.2	194091	8	ATF19F18	ATF19F18	Arabidopp
37	57.6	6.2	128961	8	XLCYCLIND1	XLCYCLIND1	A.laevis m
38	57.6	6.2	195921	8	AR123708	AR123708	Sequence
39	55.6	6.0	91740	8	ATF7520	ATF7520	Sequence
40	55.6	6.0	196339	8	F205	F205	Sequence
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42	48	5.2	1215	6			
43	47	5.1	87581	8			
44	48	5.0	114505	8			
45	46.8	5.0	114505	8			

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Db	418	TTACCAATGAACCTACTTGGATCCATTCTTATGCGTTCATGATTTGCCCTAGTGGCAAGCT	477
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Db	538	GAAGTTCCAATGTTGATAGATCTTTCAGAGTTGGAGATCTCAGTTGTGTTTGAGGCTAAA	597
Oy	481	TCAGTCCAAAGATGAGAGCTTTTGGTGTGAACAAATTTGAATGAGATTGAGAGCAATA	540
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Oy	541	ACTCCATGCTCATCAATAGATATTTCCTGAGAAAGTGAATGATATGATCAAGACCA	600
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Oy	601	TCCAACACATTTGATATGTAGATCTTTCACAAGTATAGCCAGCAACCAAAAGTATTGAC	660
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Oy	661	TTTTTTGGAGTTTAACCTTCTGAAAGCTGCTGCTGCTGTGGCACTTTCGTTTGTGAGAA	720
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Db	958	ACACCAATGGGGTTTTAGAGATATGCGGCTTGTGTTTACGTTTAAAGACCATGATTTCT	101
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Db	1018	TCCTTCTCTTATACACATCTTTCTTAA	1044
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LOCUS	AB85057	1284 bp	DNA
DEFINITION	Sequence 1 from Patent WO9842851.	PAT	21-JAN-2000
ACCESSION	AB85057		
VERSION	AB85057.1	GI:6733798	
KEYWORDS	Common tobacco.		
SOURCE	Nicotiana tabacum		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; eusterids I; Solanales; Solanaceae; Nicotiana.		
REFERENCE	Murray, J. A.		
AUTHORS	PLANTS WITH MODIFIED GROWTH		
TITLE	Patent: WO 9842851-A 1 01-OCT-1998;		
JOURNAL	MURRAY JAMES AUGUSTUS; HENRY (GB); UNIV CAMBRIDGE TECH (GB)		
FEATURES	Location/Qualifiers		
SOURCE	1..1284		
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[illegible]

JOURNAL Submitted (07-OCT-1998) Murray J.A.H., Institute of Biotechnology,
University of Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
REFERENCE 2 (bases 1 to 1284)
AUTHORS Sorrell,D.A., Combettes,B., Chaubet-Gillot,N., Gigot,C. and
Murray,J.A.
TITLE Distinct cyclin D genes show mitotic accumulation or constant
level of transcripts in tobacco bright yellow-2 cells
JOURNAL Plant Physiol. 119 (1), 343-352 (1999)
MEDLINE 99097070
FEATURES
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location/Qualifiers
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PLVLDVQVDPKFEFEGKTIOREMLVLSTLRKMQAVPYEIDYEMKMKNDIOPS
RPLISGMOLIIISRLIDLEFRSESLASVAMSSGRTOKADIDKAPCFTHIDK
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Matches 466; Conservative 0; Mismatches 208; Indels 9; Gaps 3;
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DB 365 AGTGAAGATTGCTGAGTTTATGTCAGAAAGGAATGAGATTTTGCCTAAGATGAT 424
QY 187 TACATCAAGAGCTTGAAGTGAAGTTGATTTAAATGTTGGAAGAAGATGCCCTC 246
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DB 425 TAGTGAAGAGATTGAGAGTGAAGTTGGATTGAGTGT--GAGAAAGAGAGCTCTT 481
QY 247 AATTGATTGGAAGGCTTGTGAAGACACAGTTTGGACCAATGCTTTGCTTGAAGA 306
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DB 482 GATTGATTGGAAGGCTCATATGCATATGATTTGGAGAGCTGATTTGTTGTTGTCG 541
QY 307 ATGACTACTTGGAGTCTTATGCTGTTGATGATTTGCCAAGTGGCAAGTTGGATA 366
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DB 542 ATAAATTAATCTGATCGATTTCTATCTCTGATGATTTGCCAAGATTAATCTGGACA 601
QY 367 TTGCACTTTGGGCTGCTGTTTATCATGTCGACCAAAATTTGAAGAACTGAAGTT 426
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DB 602 GTGCACTTTGTAAGCTGCTGCTATCATCTTGAAGCCAAATTTGAATTAATGTT 661
QY 427 CCAATGTTGATAGATCTTCAGTGGAGATCTTCAGTTTGTGTTGAGGCTAAATCAGTC 486
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DB 662 CTTTGAATGTTGATTTAGGTAGGAGATCCCAATTTGTTTGAAGGCAAAACTATA 721
QY 487 CAAAGATGAGACTTTTGGTGTGTAACAATTTGAATGAGATTGAGACATAACTCCA 546
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DB 722 CAAAGATGAGACTTTTGGTGTGTAACAATTTGAATGAGATTGAGACATAACTCCA 781
QY 547 TGCCTATCATAGATATTCTCTGAGAAAGATGAATTAATGATCAAGAACCTCAAC 606

DB 782 TACACATTCATGATTAATTTTATGAGAAAGATG---AATGGTATCAAAATCCCATCTCCG 838
QY 607 ACATGTATATCTGATCATATTCACAGTATAGCCAGACACCAAGATTTGACTTTTG 666
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DB 839 CCGTGTGATTTCTCGANCAATGACACGATATTAAGATATATAAGATTTGATTTCTTG 898
QY 667 GATTTAGACCTTTCTAAGCTGCTGCTGCTGGACACTTTGTTGTTGAGAAATTCAG 726
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DB 899 GAATTCAGGCTTCTCAAAATTCGACATCATGCGCAATGCTGTTTCAAGGGGAAATACAA 958
QY 727 AGATACACTTTGACACAGCTCTTCTCCCTTCCTTCCTCACTACTCAAAAGAGAGA 786
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DB 959 GCAAAGACATTTATATA---GGCATGCTTCTGCTTCTATACACTTACAGCAAGGTAGA 1015
QY 787 GTGACAGATATGAGGAATGAT 809
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DB 1016 GTGCAGAGATGTTGTAAGTAT 1038
RESULT 5
ATCD2
LOCUS 1650 bp mRNA PLN 25-MAR-1998
DEFINITION A.thaliana mRNA for cyclin delta-2 (CycD2).
ACCESSION X83370
VERSION X83370.1 GI:2995131
KEYWORDS CycD2; cyclin; cyclin D2; cyclin delta-2.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 1650)
Sonl,R., Carmichael,J.P., Shah,Z.H. and Murray,J.A.
A family of cyclin D homologs from plants differentially controlled
by growth regulators and containing the conserved retinoblastoma
protein interaction motif
Plant Cell 7 (1), 85-103 (1995)
95210930
2 (bases 1 to 1650)
Murray,J.A.H.
Direct Submission
Submitted (08-DEC-1994) J.A.H. Murray, Inst. of Biotechn., Univ. of
Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
Revised by [3]
3 (bases 1 to 1650)
Murray,J.A.H.
Direct Submission
Submitted (07-JUN-1996) J.A.H. Murray, Inst. of Biotechn., Univ. of
Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
Revised by [4]
4 (bases 1 to 1650)
Murray,J.A.H.
Direct Submission
Submitted (19-MAR-1998) J.A.H. Murray, Inst. of Biotechn., Univ. of
Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
On Mar 28, 1998 this sequence version replaced gi:1402895.
COMMENT
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Query Match      28.7%; Score 266; DB 8; Length 1650;
Best Local Similarity 63.5%; Pred. No. 2.8e-56;
Matches 461; Conservative 0; Mismatches 250; Indels 15; Gaps 3;

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571 AGAAGATGATTAATTTGATCAAGACATCCACATTTGATTTAGATTTACAA 630
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RESULT      6
LOCUS      AB011479/c
DEFINITION      Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MNAS5.
ACCESSION      AB011479 BA000015
VERSION      AB011479.1 GI:2924729
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (sites)
Kaneko,T., Kotani,H., Nakamura,Y., Sato,S., Asamizu,E., Miyajima,N.
and Tabata,S.
Structural analysis of Arabidopsis thaliana chromosome 5. V.
Sequence features of the regions of 1,381,565 bp covered by twenty
one physically assigned P1 and TAC clones
DNA Res. 5 (2), 131-145 (1998)
98344145
2 (bases 1 to 88356)
Nakamura,Y.
Direct Submission
Submitted (02-MAR-1998) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:yinakam@kazusa.or.jp,
Tel:81-438-52-3935, Fax:81-438-52-3934)
Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd-graph.cgi?c=MNAS5
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS Technical University of
Denmark, http://www.cbs.dtu.dk/services/netgene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://grem1n1.zoool.iastate.edu/cgi-bin/dsp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire inset of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
The 5' clone is MON23 and the 3' clone is K1904.
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/evidence=not_experimental
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OMEDALIEDGSLIEDGVGHASSTAERKRLGVEYKALEKNEPFDNKLPEERYKL
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Query Match 28.2% Score 261.2; DB 8; Length 88356;
Best local similarity 98.9%; Pred. No. 5.7e-55;
Matches 263; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGCAGAGAAATCTGAAGTCTTTATGTACAGAGAGCAAGTGTGATGAG 60
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DB 55649 ATGGCAGAGGAAATCTGAAGTCTTTATGTACAGAGAGCAAGTGTGATGAG 55590
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QY 61 GGCATGATTTGTGACGAACCTCCGATTTGATTCCTCAGATGGGTTTTCTCAA 120
|||||
DB 55589 GGCATGATTTGTGACGAACCTCCGATTTGATTCCTCAGATGGGTTTTCTCAA 55530
|||||
QY 121 TCGGACACTGAGAGATATATCATGTGATGGTGGAGAGAGACACATTTGCCAAGT 180
|||||

Db 55529 TCGGAGAGTGGAGGAGATTATCATGGAGATGTTGGGAGGAAGAGAACACACATTTCGCAAGT 55470

Oy 181 GATGATTACATCAGAGACCTTAGAAGTGGAGATTTGGATTGGATTGGGAAGAGAGAT 240

Db 55469 GATGATTACATCAGAGACCTTAGAAGTGGAGATTTGGATTGGATTGGGAAGAGAGAT 55410

Oy 241 GCCCATTGGATTGGGAAGCTTG 266

Db 55409 GCCCATTGGATTGGGAAGCTTG 55384

RESULT 7

CRCYD

LOCUS CRCYD 1699 bp mRNA PLN

DEFINITION C.rubrum mRNA for cyclin-D like protein.

ACCESSION Y10162

VERSION Y10162.1 GI:1770189

KEYWORDS cyclin gene; cyclin-D like protein.

SOURCE red goosefoot.

ORGANISM Chenopodium rubrum

Chenopodium rubrum

Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Chenopodium.

1 (bases 1 to 1699)

Renz,A.

REFERENCE Direct Submission

TITLE Submitted (18-DEC-1996) A. Renz, Lehrstuhl fuer

AUTHORS Pflanzenphysiologie, Universitaet Bayreuth, Universitaetsstr. 30,

JOURNAL 95447 Bayreuth, FRG

2 (bases 1 to 1699)

Renz,A., Fountaine,M. and Beck,E.

REFERENCE Nucleotide sequence of a cDNA encoding a D-type cyclin from a

AUTHORS photoautotrophic cell suspension culture of Chenopodium rubrum L

TITLE Plant Physiol. In press

JOURNAL location/qualifiers

FEATURES

SOURCE 1..1699

/organism="Chenopodium rubrum"

/db_xref="taxon:3560"

/dev_stage="7 day old culture"

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FLVLSGDKMPSKSLIDFOALDILSTIKGIDLMFRSEIAAAVAISVTOOTQIVET

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BASE COUNT 554 a 283 c 308 g 552 t 2 others

ORIGIN

Query Match 27.9%; Score 258.2; DB 8; Length 1699;

Best Local Similarity 64.0%; Pred. No. 2.5e-54;

Matches 440; Conservative 0; Mismatches 236; Indels 9; Gaps 3;

Oy 123 GGAGAGTGGAGGAGATTATCATGGAGATGTTGGGAGAGAGAGACGATTTCGCAAGTGA 182

Db 603 GGCAATATCATGAGTGTTCGGCTTCCTTGTTGACATGAAGACAAATTTTCGTGGCTCT 662

Oy 183 TCATTACATCAAGACACTTAGAAGTGGAGAGATTGGATTGGATTGGGAAGAGAGATGC 242

Query Match	Best Local Similarity	Score	DB	Length
Matches 364: Conservative	59.88	Pred. No. 4.4e-38;		
	0	Matches. 236;		
		Indels 9;		
		Gaps 2		

QY	147	GATGTGGGGAAGGAGGAGGACGATTTTCCCAAGTATGATTACATCAAGAGACT	-----	200
Db	528	GCTCGTGGAGGAAGAGGAGTGGAGACATATCCCGCGAGGCGGATTCCTCCAGAGCTGCAGCC		587
QY	201	TAGAAGTGGAGATTTTGATTTGAATGTGGAGAAGAGATGCCCTCAATTCGATTTGGAA		260
Db	588	ACGGCATGTGGACCTGATTTTGGCGCGCGTCCAGGAAGAGCGCATGATTTGGATTTGGAA		647
QY	261	GGCTGTGGAAGTACACCACTTTGGACCATTTGTGTTTTGCTTACCAATGACTTTGGGA		320
Db	648	GGTCATTTGAGCATTCATTTTGGACCGTTCACGTCGCCGTTTTGTCTGTGAACATCTCGA		707
QY	321	TGCAATCTTATGCGTTGATTTGAGTTGGCCCTAGTGGCAAGGTTGGATATTTGAGTTGGC		380
Db	708	TGATTTCTCTCCACAGTATGAGTTCCCTCGAAGGAGAGCTTGGATGACTGATGCTTTGGC		767
QY	381	TGTGCTTGTATTCATTTGGCAGCCAAATTTGAAGAAGACTGAATTCATTTGTGATAGA		440
Db	768	ACTGCTCTGCTTGTCTTTGGCTTGGAAATTCGAGACACTTTTGTGCACTCCCTTGGGA		827
QY	441	TCTTTAGCTTGGAGATCTCTCACTTTGTGTTGAGGCTAAATCAGTCCAAAGATGAGCT		500
Db	828	TTTTGAGGTAGCGGAGGCAAAATTTGTTTTTGAAGGAGAGACCATAAAGATGGAGCT		887
QY	501	TTTTGCTTTGAACAATTTGAATGAGATGAGATTTGAGAGCAATATCTCCATTCATCTAG		560
Db	888	TTCTGTGCTTAAGCACCTTTAAAGTGGAGATGATGATGCTTATCTGCTTCTGCTTTGTGA		947
QY	561	ATATTTTCTTGAGAAAGATGATTAATGTGATCAAGAACCAATCCACATATTCATCTAG		620
Db	948	ATACTTTCTTCATTAATGATGTA---TCATGTGTGCACCTCTCTTGGTTCGACGCTCTCG		1004
QY	621	ATCATTTACAGTATGATGACGACACACCAAAAGTATTTGACTTTTGGAGTTAGACCTTC		680
Db	1005	CTCTTGGAGACCTTGTCTTTGAGACACCCGTAAGAGTGTGATTTGTGTATTCAGACCTTC		1064
QY	681	TGAACCTCTCTGCTGTGGCAGCTTCTGTGTTTTCGAGATTTGCACAGATACACTTTGA		740
Db	1065	CGAATTTCTCTCCAGTGTGGACTTGTCTGTATTCGGGCAATGCAGAGATTTGTGAATTGA		1124
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Db	1125	GAGACTCTC 1133		
RESULT	9			
REFERENCE	AF12B17			
LOCUS	113053 bp	DNA	PLN	28-APR-2000
DEFINITION	Arabidopsis thaliana DNA chromosome 5, BAC clone F12B17 (ESSA project).			
ACCESSION	AF12B17			
VERSION	AJ353995			
KEYWORDS	AJ353995.1	GI:7671438		
SOURCE				
ORGANISM	thale cress.			
	Arabidopsis thaliana			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids II; Brassicales; Brassicaceae; Arabidopsis.			
REFERENCE	1 (bases 1 to 113053)			
AUTHORS	Bevan, M., Bancroft, I., Mewes, H.W., Rudd, S., Lemcke, K. and Meyer, K.F.X.			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 113053)			
AUTHORS	EU Arabidopsis sequencing project.			
TITLE	Direct Submission			
JOURNAL	Submitted (28-APR-2000) MIPs, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemcke@mp.biochem.mpg.de, mayere@mp.biochem.mpg.de Project Coordinator: John Innes Centre, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk			
COMMENT	Information on performance and analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4			

[illegible]

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SDWVVLNDEKRDIDSEOMELLDGADNSGSRISFCIGAYGHGTQVRRANVTIR
LSSVNLHQIALVLMELQLYRSWTLKQCNVHH"
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/note="strong similarity to cytochrome P450, Helianthus tuberosus, EMBL:HTCYP81L"
/codon_start=1

Query Match 16.0%; Score 148.2; DB 8; Length 113053;
Best Local Similarity 81.8%; Pred. No. 1.2e-26;
Matches 171; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 446 AGGTGGAGATCTCAGTTGTTGTTGAGGCTAAATCAGTCCAAAGATGAGCTTTGG 505
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DB 83236 AGTTGAGCTCCATGCTTCGTTGAGCTAAATCAGTCCAAAGATGAGCTTTGG 83295
QY 506 TCTTGACAAATTTGAATGAGATGAGAGCAATACATTCATCATTAAGATATT 565
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DB 83296 TGTGAACTATTGAGATGAGGAGTACGGGAGTACCGGCTTACGTTAGATTACT 83355
QY 566 TCCTGAGAAAGATGAGTAATGTGATCAGAACCATCCACATTTAGATATCTAGTCAT 625
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DB 83356 TCCTGAGTAAGATCAATGCTATGATCAAGAACCATGACATTTGTAAGTACTAC 83415
QY 626 TACAAGTATAGCCAGCACACCAAAAGGT 654
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DB 83416 TACAAGTATAGCCAGCACCAAAAGGT 83444

RESULT 10
A85058 1679 bp DNA PAT 21-JAN-2000
LOCUS A85058
DEFINITION Sequence 2 from Patent WO9842851.
ACCESSION A85058
VERSION A85058.1 GI:6733799
KEYWORDS
SOURCE
ORGANISM common tobacco.
Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
REFERENCE
AUTHORS Murray,J.A.
TITLE PLANTS WITH MODIFIED GROWTH
JOURNAL Patent: WO 9842851-A 2 01-OCT-1998;
MURRAY JAMES AUGUSTUS HENRY (GB); UNIV CAMBRIDGE TECH (GB)
FEATURES
source location/qualifiers
1..1679
/organism="Nicotiana tabacum"
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BASE COUNT 537 a 281 c 293 g 568 t
ORIGIN

Db 913 TTCGACGTATATGCCCTCCTGTAATGGCCACTGCATAATTAGCTTCACGTTATTCATCA 972

Oy 718 GAATTGCAGAGAGTACACTTTGACAACACTCTTCCTTCCTCTTTTCTCACTACTTCAA 777
+ + + + +
Db 973 GTTAGCGCTTGTAATTTCTGTTGACTACCAAAATCAACTCTTGGGGGTTCTCAAAATTAAC 1032

Oy 778 AAGGAGAGATGTAGACATAGGGAATATCATAGAGACTGATGGCTCAGACTTATATTCA 837
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Db 1033 AAGGAGAAAGTGAATAAATTTGCTTGAACTCATATCAGAAGTGTTGTTAACCCCATTTCA 1092

Oy 838 CAACACCCTAA 848
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Db 1093 CACAACGCCAA 1103

RESULT 12
AMA250397

LOCUS AMA250397 1140 bp mRNA PLN 15-NOV-1999

DEFINITION Antlirrhinum majus partial mRNA for cyclin D3a (cyd3a gene).

ACCESSION AJ250397

VERSION AJ250397.1 GI:6448481

KEYWORDS cyd3a gene; cyclin D3a.

SOURCE snapdragon.

ORGANISM Antlirrhinum majus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;
Asterales; euasterids I; Lamiales; Veronicaceae; Antlirrhinum.
1 (bases 1 to 1140)
Gaudin,V., Lunness,P., Fobert,P., Towers,M., Riou-Khamlich,I.C.,
Murray,J.J., Coen,E. and Doonan,J.H.:
The expression of D-cyclin genes define distinct developmental
zones in Antlirrhinum apical meristems and is locally regulated by
the cycloidea gene
unpublished

TITLE 2 (bases 1 to 1140)

JOURNAL Doonan,J.H.

REFERENCE Direct Submission

AUTHORS Submitted (18-OCT-1999) Doonan J.H., Cell Biology, John Innes

JOURNAL Centre, Colney Lane, Norwich, NR4 7UH, UNITED KINGDOM

FEATURES
source location/Qualifiers
1..1140
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/db_xref="taxon:4151"
/dev_stage="flower spike"
10..1139
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/protein_id="CAB61222.1"
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BASE COUNT 332 a 223 c 237 g 348 t

ORIGIN

Query Match 13.6% Score 126.2 DB 8 Length 1140;
Best Local Similarity 60.2% Pred. No. 3e-21;
Matches 209; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

Oy 233 AGAAGATGCCCTCAATTGGATTGGAAGCGTGTGAAGTACACACAGTTGGACATTG 291
+ + + + +
Db 368 ACAGATGAGCGCTGTGAATGATGTTTAAGTCATCGGTACTATCTTTCTCTCTC 427
+ + + + +

Oy 292 TCTTTTTCGCTTAGCANCTACTTGGATCGATTCTTATCGGTCATGANTTGGCTAGT 351
+ + + + +

Db	428	ACTGCGGTTCTTGCAAGTTAACTATTGGATTGGATTTCTATGCACAACTTCACGTTTCAACAA	487
QY	352	GGCAAAAGGTGGAAATATTCAGTGTGGCTGTGGCTGTATTCATTTGCGACCAAAAT	411
Db	488	GATTAAGCATGGATGTATTCAGTGTGGCTGTGGCTGTATTCATTTGCGACCAAAAT	547
QY	412	GAGAACTGAAGTTCCAAATGTTGATATCTTCAGGTTGGAGATCCACGTTTGTGTT	471
Db	548	GAGAACTGAAGTTCCAAATGTTGATATCTTCAGGTTGGAGATCCACGTTTGTGTT	607
QY	472	GAGCTAATATAGTCCAAAGATGGAGCTTTTGGCTTGGACAAATTCGAATGGAGATTG	531
Db	608	GAGCTAATATAGTCCAAAGATGGAGCTTTTGGCTTGGACAAATTCGAATGGAGATTG	667
QY	532	AGAGCAATTAATCTCCATGCTATACATTAAGATATTTCTTGAGAAAGAT	578
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RESULT	13		
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DEFINITION	Sequence 5 from Patent WO9842851.		PAT
ACCESSION	AB5061		21-JAN-2000
VERSION	AB5061.1	GI:6733802	
KEYWORDS			
SOURCE	Helianthus tuberosus.		
ORGANISM	Helianthus tuberosus		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae; Heliantheae; Helianthus.		
AUTHORS	1 (bases 1 to 1414)		
TITLE	Murray,J.A.		
JOURNAL	PLANTS WITH MODIFIED GROWTH		
FEATURES	Patent: WO 9842851-A 5 01-OCT-1998;		
source	MURRAY JAMES AUGUSTUS HENRY (GB); UNIV CAMBRIDGE TECH (GB)		
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Matches 218; Conservative	0;	Mismatches 153;	Indels 0; Gaps 0;
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Db	377	ACCTCTTACAGCCATTATAGCCATCAATATATCTTATAGATTCTTCTTACGCTCATTT	436
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Db	437	TCAGAGAGTAAACCTTGATATTCACACTGTGCTGTAGTGTCTCTCTTTAGCTGC	496
QY	405	CAAAATTTGAAGAACTGGAATTCACATGTTGGATAGATCTTCAGTTGGAGATCCACATT	464
Db	497	TAAATTTGAAGAACTGGAATTCACATGTTGGATAGATCTTCAGTTGGAGATCCACATT	556
QY	465	TGTGTTTGAAGCTTAATCAGTCCAAAGATGAGCTTTTGGTGTGAACAAATGAATG	524
Db	557	CTTGTGTTGAGCTTAAACATACATAAAATGAGCTTTTGGTGTGAATGCAACTTGAATG	616
QY	525	GAGATTGAGAGCAATTAATCCATGCTCATACATTAAGATATTTCCGGAAGATGAGTAA	584
Db	617	GAGATTGAGAGCAATTAATCCATGCTCATACATTTCTTATCATCAATTTGAAGAGGCTTGATT	676

OY 585 ATGATCAAG 595
Db 677 AACTGATCATG 687

RESULT 14

AB015222 1487 bp mRNA PLN 02-APR-1999
LOCUS Nicotiana tabacum Ntncyd3-1 mRNA, complete cds.
DEFINITION AB015222
AB015222.1 GI:4586800
VERSION Ntncyd3-1.
KEYWORDS Nicotiana tabacum cell_line:BY-2 cDNA to mRNA.
SOURCE Nicotiana
ORGANISM Nicotiana tabacum

REFERENCE Eukariyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 1487)

REFERENCE Sekine/M.
AUTHORS Cell cycle regulated gene

JOURNAL Published only in Database (1999) In press
REFERENCE 2 (bases 1 to 1487)

AUTHORS Sekine/M.
TITLE Direct Submission
JOURNAL Submitted (03-JUN-1998) to the DDBJ/EMBL/Genbank databases. Masami

Sekine, Nara Institute of Science and Technology, Graduate School
of Biological Sciences; Takayama 8916-5, Ikoma, Nara 630-0101,
Japan (E-mail: sekine@nibs.ist-nara.ac.jp, Tel:+81-743-72-5462,
Fax:+81-743-72-5469)
Sequence updated (19-Aug-1998).

FEATURES Location/Qualifiers
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CDS 136..1242
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1487

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ORIGIN

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Best Local Similarity 60.5%; Pred. No. 3.4e-21;

Matches 207; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

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Db 398 GTAAGAGCTGTGAATGATCTTAAGTAATGCTCATTTATGATTCGCAACATTC 457

OY 293 GTTTTGCTTACGAATGACTTGTGATGATTTATCGGTTTCATGATTTGCC 352

Db 458 CTCCTATTCTTCTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 517

OY 353 GCAAGTGTGATATGATTTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGG 412

Db 518 ATTAGCTTGATGATTCACCTGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTG 577

OY 413 AGAAGCTGAAGTTCATGTTGATGATCTGAGTTGGAGATCCGATTTGTTGTTG 472

Db 578 AGAAGCTGAAGTTCCTCTCTTTTGACCTCCAGTCGACGATCCAAATATGTTTG 637

OY 473 AGGCTAATGATTCGCAAGAGATGAGCTTTGGTGTGAACAAATGAATGAGATTTGA 532

Db 638 AGGCAAACTAATTCAAAGATGAGCTTTGGTGTGAATGCTCTTTAAAGTGAAGATGA 697

OY 533 GAGCAATGATTCGATGCTCATACATTAAGATATTTCCGAGAA 574

Db 698 ATCCGTAAACCCACCTTCTATTGTTGATCATATATAAAGAA 739

RESULT 15

AB5060 1788 bp DNA PAT 21-JAN-2000
LOCUS Helianthus tuberosus
DEFINITION Sequence 4 from Patent WO9842851.
AB5060
AB5060.1 GI:6733801
VERSION
KEYWORDS
SOURCE Helianthus tuberosus.
ORGANISM Helianthus tuberosus

REFERENCE Eukariyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.
1 (bases 1 to 1788)

AUTHORS Murray,J.A.
TITLE PLANTS WITH MODIFIED GROWTH
JOURNAL Patent: WO 9842851-A 4 01-OCT-1998;
MURRAY JAMES AUGUSTUS HENRY (GB); UNIV CAMBRIDGE TECH (GB)

FEATURES Location/Qualifiers
source 1..1788
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/db_xref="taxon:4233"

BASE COUNT 511 a 386 c 387 g 504 t
ORIGIN

Query Match 13.3%; Score 123.2; DB 6; Length 1788;
Best Local Similarity 52.1%; Pred. No. 1.7e-20;

Matches 335; Conservative 0; Mismatches 293; Indels 6; Gaps 2;

OY 124 GAGAGTGAAGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 183

Db 276 GATTTGATGATTCATGATCCGCGGATTTATAGACAGAGAGAAAGTTCGTCAGAAATC 335

OY 184 GATTACATCAAGAGACTTGAAGTGAAGATTTGATTTGAATGTTGGAAGACATGCC 243

Db 336 GATTAGCTGAGAGATTTCAATGCAAGTTCGAT---GTTCTGCTAGAGAAAGATCG 392

OY 244 CTCATTTGGATTTGGAAGCTTGTGAAGTACACCACTTTGGACCATTTGTTTGTCTTA 303

Db 393 GTTGCTGATCTTAAAGGCAACGGTTTACGATTCACCGTTGACGGCTACCTC 452

OY 304 GCAATGACTACTTGGATGATTTCTTATCGGTTTCATGATTTGGCTGATGGAAGTTGG 363

Db 453 TCGGTAACTATGATGATGATTTGATTCATGATTTGCGGCTGCTCCGGTGGCAATGGCTGG 512

OY 364 AATTTGCACTTTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 423

Db 513 CCTTCAACTCTTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 572

OY 424 GTTCCATGTTGATTAATGTTCAAGTTGAGATCCCACTGTTGTGTTTACGCTTAATGA 483

Db 573 ATTCTCTTATTTCTTATCTCAGGTTGAAGGTGCAAAATTAATTTTGAAGCCAAAGAA 632

OY 484 GTTCAAGATGAGAGCTTTGCTGTGAACAAATTAATTAATTAATTAATTAATTAATTA 543

Db 633 ATCCGAAGATGAGAGTTTCTTGTGCTTACTGTTTGGATTTGAGATCAAGATCCGTTACA 692

OY 544 CCATGCTCATATACATATTTCTGAGAAAGATGATTAATTTGATCAAGAACCATCC 603

Db 693 CGTTTAGCTTAATAGCGCTTCTTTTGGACAAATGATGATTCATGATGATATACGGGT 752


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OY 604 AACACATTGATATCTAGATCATTTACAGTGATAGCCAGCACCAAGCATTTGACTTT 663
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Db 753 TTC--CTATCTCAAGGCAACAAATATTCCTCAATATTCAGAAAGCTAGTTTA 809
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Db 810 CTTGAGTATTTGGCCATCATGTATGTGCTGCGCAACAATACTTTGTGCAGCAAGTGATCTT 869
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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Title: US-09-530-209A-1

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Gapop 10.0 , Gapext 1.0

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	923.8	99.7	1287	21	AAAC48940
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4	302.2	32.6	1284	19	AAV33884
5	193.4	20.9	1077	21	AAZ94582
6	193.4	20.9	1846	19	AAV33889
7	193.4	20.9	1861	21	AAZ94581
8	156.8	16.9	1173	21	AAZ94583
9	140.6	15.2	1932	20	AAZ19961
10	127.8	13.8	1679	19	AAV33885
11	126.2	13.6	1414	19	AAV33888

12	123.2	13.3	1788	19	AAV33887
13	118.4	12.8	1431	19	AAV33886
14	116	12.5	1311	21	AAAC40202
15	111.2	12.0	1337	21	AAAC42423
16	104.2	11.2	1356	21	AAAC51463
17	104.2	11.2	1358	21	AAAC35723
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ALIGNMENTS

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XX
AC AAV36897;
XX
DT 16-JUL-1999 (first entry)
XX
DE Mitogenic cyclin CYCD4 coding sequence.
XX
DT Mitogenic cyclin: CYCD4; modulator; plant cell cycle; growth inhibitor;
XX
KW plant cell division; cell growth; regulator; cell proliferation;
KW growth regulator; herbicide; cell division progression; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO9922002-A1.
XX
PD 06-MAY-1999.
XX
PF 23-OCT-1998; 98WO-EP06749.
XX
PR 24-OCT-1997; 97EP-0203303.
XX
PA (CROP-) CROPEDESIGN NV.
XX
PI De Almeida J, De Veylder L, Inze D;
XX
DR WPI: 1999-312966/26.
XX
PT P-PSDB: AA114071.
XX
PS DNA sequence encoding a mitogenic cyclin
Claim 1: Page 47-49; 57pp; English.

XX This sequence encodes the mitogenic cyclin, CYCD4, of the invention.
CC The DNA sequence, vectors containing it, protein encoded by it, or
CC antibodies recognising the protein can be used for modulating plant cell
CC cycle, plant cell division and/or growth, for influencing the activity of
CC mitogenic cyclin in a plant cell, as positive or negative regulator of
CC cell proliferation, for modifying the growth inhibition caused by
CC environmental stress conditions, or for use in a screening method for the
CC identification of inhibitors or activators of cell cycle proteins. A
CC compound which is an activator or inhibitor of the mitogenic cyclin can
CC be used as a growth regulator and/or herbicide. The proteins can also be
CC used to influence cell division progression in yeast, mammals and
CC insects.

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Best Local Similarity 100.0%; Pred. No. 9.8e-253;

Matches 927; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 421 gaagttccaaatgttgatagatcttcaggttgagatccacagtttgttggagctaaa 480
QY 481 TCAGTCCAAAGATGAGGCTTTTGTGTGAACAAATGAATGAGATTGAGAGCAATA 540
Db 481 tcagtccaaagatgaggcttttgtgtgaacaaatgaaatggagattggagaata 540
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QY 781 GAGAGAGTGAGAGATAGAGGGAATGATGAGAGTGAAGCTCAGACTTATGTTCAAA 840
Db 781 gagaagtgagaagaagataggggaatgatagagatgagatgagctcactatgttcaaa 840
QY 841 ACACCCCAATGGGTTTAAAGATGAGGCTTGTGTTTACGTTTAAAGACCATGATTC 900
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AC AAC48940;
XX

DT 18-OCT-2000 (first entry)
XX

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 59332.

XX Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.

OS Arabidopsis thaliana.

PN EP1033405-A2.

XX
PD 06-SEP-2000.

XX
PF 25-FEB-2000; 2000EP-0301439.

XX
PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0130891.

PR 30-APR-1999; 99US-0132048.

PR 30-APR-1999; 99US-0132407.

PR 04-MAY-1999; 99US-0132484.

PR 05-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

PR 06-MAY-1999; 99US-0132487.

PR 07-MAY-1999; 99US-0132863.

PR 11-MAY-1999; 99US-0134256.

PR 14-MAY-1999; 99US-0134219.

PR 14-MAY-1999; 99US-0134221.

PR 14-MAY-1999; 99US-0134370.

PR 18-MAY-1999; 99US-0134768.

PR 19-MAY-1999; 99US-0134941.

PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.

PR 24-MAY-1999; 99US-0135629.

PR 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999; 99US-0136392.

PR 28-MAY-1999; 99US-0136782.

PR 01-JUN-1999; 99US-0137222.

PR 03-JUN-1999; 99US-0137528.

PR 04-JUN-1999; 99US-0137502.

PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
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PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141844.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
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PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
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PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
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PR 02-AUG-1999; 99US-0146389.
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PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.

PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147933.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
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PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
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PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153738.
PR 15-SEP-1999; 99US-0154018.
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PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
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PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
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PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 99.7%; Score 923.8; DB 21; Length 1287;
Best Local Similarity 99.8%; Pred. No. 9e-252;
Matches 925; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGCAGAGAAAACTAGAACTGAGTCTTTATGTACAGAGACAGCTTGATGATGAG 60
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Db 242 atggcagagaggaatctcagacacgagcttcttatgtccagagcaacgcttgagagag 301
QY 61 GGCGATGATTTTGACGAACCTCCGATTGAAAATTCGATTCCTCAGATGGGTTTCTCAA 120
|||||
Db 302 ggcattgtgtgacggaactccgattgaattcgcattccctcagatgggttttcccaa 361
QY 121 TCGAGAGGTAGAGAGATTATCATGAGAGATGTTGAGAGAGAGAGAGAGCCATTGGCCAGT 180
|||||
Db 362 tcggagagtgagagatcatcagagatggtgagagagagagagagagagagagagag 421
QY 181 GATGATTCATCAAGAGACTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 240
|||||
Db 422 gatgatctacatcagagacttaagaagtggagattggatttgatggtgagagagagat 481
QY 241 GCCCTCAATTTGATTTGGAAGGCTTGTGAAGTACACACAGTTTGGACCATTTGTTTTCG 300
|||||
Db 482 gccctcaattggatttggagagcttggagagtaacacagagtttgaccattgtttttgc 541
QY 301 TTAGCATGAACTACTTGGATTCGATTCCTATCGGTTTCATGATTTGCCCTAGTCCAAAGCT 360
|||||
Db 542 ttgacatgagacacttgatcgtatctctatcgttcatgatttgcttagtggcaaggt 601
QY 361 TGGATATTGAGTTGCTTGCTGGCTGCTGCTTTTATCATTTGGCAGCCAAAAATTTGAAGAACT 420
|||||
Db 602 tggatattgagtggttggtggtgtggtgtgttctatcttgccagccaaatctgagaaact 661
QY 421 GAAGTCCAAATGTTGATAGATCTTCAGGTTGAGAGATCCATGTTTGTTGAGCTTAA 480
|||||
Db 662 gaagttccaatgtgtgtagtcttcaggttggagatccctcaggttggtttggagctaa 721
QY 481 TCAGTCCAAAGATGAGAGCTTTGGTGTGAGCAAAATTTGAATGGAGATTGAGAGCAATA 540
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Db 722 tcagtcgaagaatgagagcttctgtgtgcaaaaatgaaatggagatggagagcaata 781
QY 541 ACTCATGCTCATACATAAGATATTTCTGAGAAAGATGATGAATGTGATCAAGAACCA 600
|||||
Db 782 actccatgtcatatacctaagataatctccctgagagaaagatgataatgtatcaagaacca 841
QY 601 TCCACACATGATATCTAGATCATTTACAAGTATGAGCAGCAACAACAAGTATTGAC 660
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Db 842 tccaacaactgtatcatcagatcatcaagaagtatgacagcacaacaaaggtattgac 901
QY 661 TTTTGGAGTTTGAAGCTTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
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Db 902 ttttggagtttgaagcttctgaaagcttgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgt 961
QY 721 TTGCAGAGAGTACACTTTGACAACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
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Db 962 ttgcagagaggtacacttgcacacacttctctctctctctctctctctctctctctctctct 1021
QY 781 GAGAGAGTAAAGATAGAGGGAATGATGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 840
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Db 1022 gagaagagtgaaagaatagaggaatgagagagagagagagagagagagagagagag 1081
QY 841 ACACCCAAATGGGGTTTAAAGATGAGGCTTGTGTTTGAAGTGAAGTGAAGTGAAGTGAAG 900
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Db 1082 acacccaaatggggttttaaagatgagagagagagagagagagagagagagagagagag 1141
QY 901 TCTTCTTTTATACATCTTCTTAA 927
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Db 1142 tcttctctatacacatcttctctaa 1168

XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 26607.
DE Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
PN EP1033405-A2.
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0125264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
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PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
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PR 20-MAY-1999; 99US-0135124.
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PR 25-MAY-1999; 99US-0135629.
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PR 28-MAY-1999; 99US-0136392.
PR 01-JUN-1999; 99US-0137282.
PR 03-JUN-1999; 99US-0137222.
PR 04-JUN-1999; 99US-0137528.
PR 07-JUN-1999; 99US-0137502.
PR 08-JUN-1999; 99US-0137724.
PR 10-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 14-JUN-1999; 99US-0138847.
PR 16-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
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PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.

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PR 26-OCT-1999: 99US-0161359.
PR 26-OCT-1999: 99US-0161360.
PR 26-OCT-1999: 99US-0161361.
PR 28-OCT-1999: 99US-0161920.
PR 28-OCT-1999: 99US-0161992.
PR 28-OCT-1999: 99US-0161993.
PR 29-OCT-1999: 99US-0162142.

Query Match 99.3%; Score 920.6; DB 21; Length 1290;
Best Local Similarity 99.6%; Pred. No. 7.3e-251;
Matches 923; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGCGAGAGAAATCTAGACACTGACTCTTTTATGTACAGAGCAACGTTGATGATGAG 60
|||||
Db 244 atggcagagagagactatagaactgagctcttltatgltacagagcaacglttgatgag 303
|||||

QY 61 GGCATGATTGTTGACGAACCTCGATTGAATTCGATTGCTGAGATGGFTTTTCGAA 120
|||||
Db 304 ggcatagtatctgtaacgaacatccgaltgaaatttcgaltccatgaatgglttcccaa 363
|||||

QY 121 TCGAGAGTGCAGAGATTATCATGAGATGCTGAGAGAGAGAGCAAGCATTTGCCAAGT 180
|||||
Db 364 tcggagagatgtagagactatcatcatgagatgtagagagagagacgacatlttgccaagt 423
|||||

QY 181 GATGATTACATCAAGAGACTTACAGAGTGCAGATTTGGATTGATGTGGAGAGAGAT 240
|||||
Db 424 gatgattacatcacaagagacttagaagtgagatttgatgtaatgttggaagaagagat 483
|||||

QY 241 GCCCTCAATTGATTGGAAAGGCTTGGAAGTACACAGTTTGACCATTTGTTTTCG 300
|||||
Db 484 gccctcaattgatttggaaggtctgtaagtaacacagcaglttgaccacattglttctgc 543
|||||

OY 585 ATGTG---ATCAAGAACCATCCACACATGATATCTAGATCATTTACAGTGTATGACCCAG 641
 DB 904 cggcgccagcagcgcgcgagagagctcgtcgtcttcgacgtccgcggaacttcttcgcg 963
 OY 642 CACAACCAAGGATTTAGCTTTTGGAGTTTGGACCTTCTGAAAGCTGCTGCTGTGGC 701
 DB 964 tgcgcgcagaggaacccgctcgtcgttcagcgcgcgcgagatccgcgcgcggttcgc 1023
 OY 702 ACTTTCTGTTTCTGGAAGATTGCAGAGACTACACTTTTGACAACTCTTCTCTCTC 760
 DB 1024 agccgcgcgtgc 1082
 RESULT 10
 AAV33885
 ID AAV33885 standard; cDNA to mRNA; 1679 BP.
 AC AAV33885;
 XX
 DT 25-JAN-1999 (first entry)
 XX
 DE N. tabacum CYCD3:1 gene.
 XX
 KM D-type cyclin; growth; plant; cell-division control; phosphorylation;
 KM CDC; Rb; retinoblastoma; germination; flowering; seed; fruit;
 KM root development; ds.
 XX
 OS Nicotiana tabacum.
 XX
 PN WO9842851-A1.
 PD 01-OCT-1998.
 XX
 PF 24-MAR-1998; 98MO-EP01701.
 XX
 PR 26-MAR-1997; 97EP-0302096.
 XX
 PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
 XX
 PI Murray JAH;
 DR WPI: 1998-532012/45.
 XX
 XX
 PT Regulating growth and structure of plants by modulating protein that
 PT controls cell division - specifically a D-type cyclin, and related
 PT chimeric genes and transformed cells and plants, used to alter
 PT growth rate, flowering, seed production etc.
 PS
 PS Claim 14; p54; 75pp; English.
 XX
 CC This sequence represents the CYCD3:1 cDNA from Nicotiana tabacum which
 CC encodes a D-type cyclin. The sequence can be used to alter the growth
 CC characteristics or architecture of plants by altering the (functional)
 CC level in the plant cells of a cell-division controlling protein that can
 CC bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin.
 CC Modulation of the cyclin gene is used to increase or decrease the growth
 CC rate, provide faster germination, reduce time to flowering, increase the
 CC number of flowers, seeds or fruits per plant, increase root development,
 CC reduce height and to delay flowering in a range of plants, e.g. legumes,
 CC grasses, maize, oilseed rape, wheat, tomato, rice, barley, sunflower,
 CC carnation, chrysanthemum, rose, tulip, etc.
 CC
 SO Sequence 1679 BP; 537 A; 281 C; 293 G; 568 T; 0 other;

Query Match 13.8%; Score 127.8; DB 19; Length 1679;
 Best Local Similarity 50.6%; Pred. No. 2.9e-26;
 Matches 309; Conservative 0; Mismatches 302; Indels 0; Gaps 0;

OY 238 GATGCCCTCAATTGATTTGGAGGCTTGTGAAGTACACCACTTTGGACCATTTGCTTTT 297
 DB 493 gattctgtgtaagtgtatttaaaagtgaatgtattatgttctctgttgcattgcgc 552

OY 298 TCGTTAGCAATGAACACTACTTGGATGCTATTCTTATCGGTTCAATGATTTGCCCTAGTGGCAAA 357
 DB 553 gtttttgccataaataacttcttgacaggttcttcgacgttcattcatatcagaagaataaa 612
 OY 358 GGTGGATATTCAGTTGTTGGCTGTGGCTTTTATCATTTGGACCCAAATTTGAAGAA 417
 DB 613 ccttgatgattcaacttgcgtcgttacttgccttcttcttgcgtcctaagtgtaagaa 672
 OY 418 ACTGAAGTTCCAAATGTTGATATCTTCAGAGTTGGAGATTCCTCAGTTGTTGGAGCT 477
 DB 673 actcaagttccttcttcttgaatttcaagtggaagatgctaataatgltgtgaagca 732
 OY 478 AATFATGTCGAAGTGAAGAGCTTTTGTGTGTAACAAATTTGAATGAGATTGAGAGCA 537
 DB 733 aaacattcacaagaatggaagcctttagtgtgttcttcaactaaagggagatgaatcca 792
 OY 538 ATTAATCTCATGCTCATATACATTAATATTTCTTGAGAAAGATGTAATGTATCAAGAA 597
 DB 793 gtgaccccaattcattcttcttgatcatatataaagaggttggtctaagaaataatatl 852
 OY 598 CCATCCACACATTTGATATCTATCATATTTCATGATAGCCGACCAACCAAGGATTT 657
 DB 853 cacttggaaattcttgaagaatgtaaaatcctcctctctatctatggtcgtatgtaga 912
 OY 658 GACTTTTGGAGCTTTAGACCTTCTGAAAGCTGCTGCTGTGGCACTTTCTGTTCTGGA 717
 DB 913 ttcgtacgttatatgcgcgtctgtatgtgcacatgaatlatgcttaacgttatatcaaa 972
 OY 718 GAATTCAGAGAGTACACTTTTGACAACTCTTCTCTCTCTTTTCTCAGTACTTCAA 777
 DB 973 gttgagccttgaattctgttgactacccaataacttcttggtgttcccaaatlaac 1032
 OY 778 AAGCAGAGCTGAAGAAGATGAGGAAATGATAGAGATGATGCGATGATGATTTCA 837
 DB 1033 aaggaagaatgtataatgtcttgaaactatcagaagtggttcttaagccattca 1092
 OY 838 CAAACACCCAA 848
 DB 1093 cacaacgcga 1103

RESULT 11
 AAV33888
 ID AAV33888 standard; cDNA to mRNA; 1414 BP.
 AC AAV33888;
 XX
 DT 25-JAN-1999 (first entry)
 XX
 DE H. tuberosus CYCD3:1 gene.
 XX
 KM D-type cyclin; growth; plant; cell-division control; phosphorylation;
 KM CDC; Rb; retinoblastoma; germination; flowering; seed; fruit;
 KM root development; ds.
 XX
 OS Helianthus tuberosus.
 XX
 PN WO9842851-A1.
 PD 01-OCT-1998.
 XX
 PF 24-MAR-1998; 98MO-EP01701.
 XX
 PR 26-MAR-1997; 97EP-0302096.
 XX
 PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
 XX
 PI Murray JAH;
 DR WPI: 1998-532012/45.
 XX
 PT Regulating growth and structure of plants by modulating protein that
 PT controls cell division - specifically a D-type cyclin, and related

PN	W09842851-A1
XX	
PD	01-OCT-1998.
XX	

Db 753 ttc---ctatccaaggcacacaacattatcctctcaatatccaagagcctagttta 809

Db 810 cttgagatattgacacatgatctgctgcacacatacttggcagcaagtatcctt 869

Oy 724 CAGAGATGACACTTGGACACTCT 747

Db 870 tctaattcactatcaatgct 893

RESULT 13

AAV33886 ID AAV33886 standard; cDNA to mRNA; 1431 BP.

AAV33886; AC AAV33886; XX 25-JAN-1999 (first entry)

DE N. tabacum CYCD3.2 gene.

DE D-type cyclin; growth; plant; cell-division control; phosphorylation; KW CDC; Rd; retinoblastoma; germination; flowering; seed; fruit; KW root development; ds.

OS Nicotiana tabacum.

XX W09842851-A1.

XX 01-OCT-1998.

PD 24-MAR-1998; 98WO-EP01701.

PF 26-MAR-1997; 97EP-0302096.

XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

PA Murray JAH:

PI WPI; 1998-532012/45.

DR Regulating growth and structure of plants by modulating protein that PT controls cell division - specifically a D-type cyclin, and related PT chimeric genes and transformed cells and plants, used to alter PT growth rate, flowering, seed production etc.

XX Claim 14; p55-56; 75pp; English.

XX This sequence represents the CYCD3.2 cDNA from Nicotiana tabacum which CC encodes a D-type cyclin. The sequence can be used to alter the growth CC characteristics or architecture of plants by altering the (functional) CC level in the plant cells of a cell-division controlling protein that can CC bind to, or phosphorylate, an Rd-like protein, such as a D-type cyclin. CC Modulation of the cyclin gene is used to increase or decrease the growth CC rate, provide faster germination, reduce time to flowering, increase the CC number of flowers, seeds or fruits per plant, increase root development, CC reduce height and to delay flowering in a range of plants, e.g. legumes, CC grasses, maize, oilseed rape, wheat, tomato, rice, barley, sunflower, CC carnation, chrysanthemum, rose, tulip, etc.

XX Sequence 1431 BP; 387 A; 267 C; 299 G; 478 T; 0 other:

Query Match 12.8%; Score 118.4; DB 19; Length 1431; Best Local Similarity 57.6%; Pred. No. 1.2e-23; Matches 212; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

Oy 207 TGGAGATTGGATTGATGTTGGAAGAGAGATCCCTCAATTGGATTGGAGCCTTG 266

Db 443 tggagatgggttlltagggaggttagaagaagagcatggatggatgttagagatc 502

Oy 267 TGAAGTACACGATTGGACCAATTGTGTTTGGCTTACGAATGAACACTGGATGATT 326

Db 503 tgcctacatgggttgcacgtacgtactgtctttagctggaatcattctgatagtt 562

Oy 327 CTTATCGGTTGATGATTGCTCAGTGGCAAGGTTGATATGCACTGTTGGCTGTGCG 386

Db 563 tgtatcgtgaccctgctcttcagaaagataagccttgatgagtgcaacttgcgcgtg 622

Oy 387 TTGTTTATCATTTGGCAGCCAAATTTGAGAAGTGAAGTTCATGATGATCTTCA 446

Db 623 ttgtcttctatcttgctgctaaagtgaagagacccacccctctctcttagactcca 682

Oy 447 GGTGGAGATCCCTCAGTTGTTGAGGCTAAATTCAGTCCAAAGATGACCTTTTGGT 506

Db 683 agtggcgtgattcaagatttglttgaggcaagactatcagaagatggaactcttgg 742

Oy 507 GTTGAAACAATTGAATGAGAGATTGAGAGCAATTAACCTCCATCATAGATATT 566

Db 743 gctccacactcttaagtgaagaaatgaatccagtgacaccacatctctatgatcat 802

Oy 567 CCTGAGAA 574

Db 803 catgagga 810

RESULT 14

AAC40202 ID AAC40202 standard; DNA; 1311 BP.

AAC40202; AC AAC40202; XX 17-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 27437.

DE Hybridisation assay; genetic mapping; gene expression control; KW protein identification; signal transduction pathway; KW metabolic pathway; promoter; termination sequence; ss.

XX Arabidopsis thaliana.

OS EPI033405-A2.

PN 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

PF 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 23-APR-1999; 99US-0130891.

PR 28-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132408.

PR 30-APR-1999; 99US-0132407.

PR 04-MAY-1999; 99US-0132484.

PR 05-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

PR 06-MAY-1999; 99US-0132487.

PR 07-MAY-1999; 99US-0132863.

PR 11-MAY-1999; 99US-0134256.

PR 11-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134219.

PR 14-MAY-1999; 99US-0134221.

PR 14-MAY-1999; 99US-0134370.

PR 18-MAY-1999; 99US-0134768.

PR 19-MAY-1999; 99US-0134941.

PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.

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PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
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PR 18-JUN-1999; 99US-0139454.
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PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139760.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
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PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
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PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.

PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147933.
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PR 13-AUG-1999; 99US-0148565.
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PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
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PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
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PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151433.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
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PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
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PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
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PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.

PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 12.5%; Score 116; DB 21; Length 1311;
Best Local Similarity 58.3%; Pred. No. 5,7e-23;
Matches 203; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

OY 210 AGATTGGATTTGATGTTGGAGAGAGATGCCCTCAATTGGATTTGGAAGCCTTGTGA 269
Db 429 agatggcttcttgcttctcttagaagaagagccttagatggcttcttagagttcaatc 488
OY 270 AGTACCCAGTTTGGACCATTTGTTTGGTTAGCAATGAATCTTGAATGATTTCTT 329
Db 489 tcatatgggttacttacttgaagcgcatactgctgtaactacttcgaagtttat 548
OY 330 ATCGGTCATATTTGCTTACTGSCAAGTTGATATTTGCAATGCTTGGCTGGCTTG 389
Db 549 gacaagataaagcttcagactgataagcatalgcatcagcttgcttgctgcttc 608
OY 390 TTTATCATTTGCAGCCAAATTTGAGAACTGAAGTCCAAATGATAGATCTCAGGT 449
Db 609 ttgctttagctgcttaagtttgaagttcaagttccatctgctttagacctcaagt 668
OY 450 TGGAGATCCTCAGTTTGTGTTGAGGCTAAATCAGTCCAAAGATGAGCTTTGCTGT 509
Db 669 ggaagaagaagatatactctttagaagcctaagacgattcaagaagaagctttagtct 728
OY 510 GAACAATTTGAATGAGATTTGAGAGCAATTAATCCTCATGCTCATACAT 557
Db 729 ttctactctcaatgagaatgcacccttgctacccaatcttcttct 776

RESULT 15

AAC42423
AAC42423 standard; DNA; 1337.BP.

XX AAC42423;

XX 17-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 35500.

XX Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

XX Arabidopsis thaliana.

OS EPI033405-A2.

PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 21-APR-1999; 99US-0130077.

PR 23-APR-1999; 99US-0130510.

PR 23-APR-1999; 99US-0130891.

PR 28-APR-1999; 99US-0131449.

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PR 30-APR-1999; 99US-0132407.

PR 04-MAY-1999; 99US-0132484.

PR 05-MAY-1999; 99US-0132485.
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PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134221.
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PR 19-MAY-1999; 99US-0134941.
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PR 27-MAY-1999; 99US-0136392.
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PR 01-JUN-1999; 99US-0137222.
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PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.

Search completed: January 21, 2002, 00:21:58
Job time: 2927 sec

b 715 tgyccngtnacnathathwsntggytnaaytnttlyt 752

Query Match	5.2%	Score 48	DB 4	Length 1215
Best Local Similarity	32.5%	Pred. No. 0.00019		
Matches 110; Conservative	60;	Mismatches 159;	Indels 9;	Gaps 2

RESULT 3
US-09-092-770-18
; Sequence 18, Application US/09092770
; patent No. 5973119

```

: GENERAL INFORMATION:
: APPLICANT: Coats, Steven R.
: APPLICANT: Bass, Michael B.
: APPLICANT: Robinson, Murray O.
: TITLE OF INVENTION: NO. 5973119el Cyclin E Genes and Proteins
: FILE REFERENCE: A-524
: CURRENT APPLICATION NUMBER: US/09/092,770
: CURRENT FILING DATE: 1997-06-05
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 18
: LENGTH: 1212
: TYPE: DNA
: ORGANISM: Mouse
: OS-09-092-770-18

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Query Match	4.7%	Score 43.6	DB 2	Length 1212
Best Local Similarity	31.4%	Pred. No. 0.0034		
Matches 106	Conservative 60	Mismatches 163	Indels 9	Gaps
QY	232	AGAACAGATGCCCTCATTTGGATTGGAAAGGCTGTGTAAGTACACCAAGTTTGGACCAATTG	291	
Db	421	mgwnsnathtytnyngaytgytytnyngaraytnygyargyntayacnytncaymngar	480	
QY	292	TGTTTTTTCCTAGCAATGAACACTTGTGGATGATCTTATTCGTTATGATTTGCTTAGT	351	
Db	481	acnttlaytngcmcargaytlttlylgaymgnttlaytelyglnaecnaraa-----Tgay	534	
QY	352	GGCAAAAGTTGGATATTGCTACTTGTGGCTGTGGCTGTTATTATCTTTGGACGCCAAATT	411	
Db	535	glnaaayaaraayalttyncaarytlnabghnahtcnsnynttlytchagwmsnaaytn	594	
QY	412	GAAAGAACTGGAAGTTCCATGCTGTGATATGATCTTCGAGTTGGAGATCCCAAGTTTGCTTT	471	
Db	595	gargarralthtygcncnaaaytncaargarttlycncntayglnaecnaryggnocntlywsm	654	
QY	472	GAGGCTAAATCAGTCCAAAGAAGGAGGCTTTTGGTTGGAAACAATTTGAATGGAGATTG	531	
Db	655	gargngnya---thynaaratgarytlnaaytthylnaargonylnaarttggarytn	711	
QY	532	AGAGCAATTAAGCTGCTCATACATTAAGATATTCCCT	569	
Db	712	tygcngtnaecnghnatwsmtnygtlytnaaytlnltlyt	749	

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RESULT 4
US-09-222-851-18
Sequence 18, Application US/09222851
Patent No. 6165753
GENERAL INFORMATION:
APPLICANT: Coats, Steven R.
APPLICANT: Bass, Michael B.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: No. 6165753el Cyclin E Genes and Proteins
FILE REFERENCE: A-524
CURRENT APPLICATION NUMBER: US/09/222,851
CURRENT FILING DATE: 1998-12-30
EARLIER APPLICATION NUMBER: 09/092,770
EARLIER FILING DATE: 1998-06-05
NUMBER OF SEQ. ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ. ID NO 18
LENGTH: 1212
TYPE: DNA
ORGANISM: Mouse
US-09-222-851-18

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Query Match	4.7%;	Score 43.6;	DB 4;	Length 1212;
Best Local Similarity	31.4%;	Pred. No. 0.0034;		
Matches 106;	Conservative 60;	Mismatches 163;	Indels 9;	Gaps 2;

[illegible]

Db 655 garingngaya---thylnaaratggarlylnaayachylnaagcylnaaratggarlyln 711
OY 532 AGAGCAATPACTCCATGCTCATATACATAGATTTTCT 569
Db 712 tgyccnglnacnglnathtwntlgyltnaaylnttlyt 749

RESULT 5

US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232.463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935.313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PTZgpt-F15
US-08-232-463-14

Query Match 4.4%; Score 40.6; DB 1: Length 7218;
Best Local Similarity 6.0%; Pred. No. 0.055;
Matches 19; Conservative 166; Mismatches 130; Indels 0; Gaps 0;
OY 3 GGCAGAGAAATCTAGACTGCTTTTATGTACAGAGACGATGATGAGG 62
Db 1339 RRR 1280
OY 63 CATGATTTGTCAGAACCTCCGATTCGATTCCTCAGATGGTTTTCTCAATC 122
Db 1279 RRR 1220
OY 123 GGAGAGTGGAGATATATGAGATGTCGAGAGAGACGACATTTGCCAGTGA 182
Db 1219 RRR 1160

OY 183 TGATTACATCAGAGACTTAGAAGTGGAGATTGGATTGAAATGTTGAAGAAGACATGC 242
Db 1159 RRR 1100
OY 243 CCTCAATGATTTGGAGAGCTTGTGAAGTACACGATTTGGACATTTGTTTTCCT 302
Db 1099 RRR 1040
OY 303 ACCAATGAACACTT 317
Db 1039 ACCTCGAATTAAT 1025

RESULT 6

US-08-306-691B-51
Sequence 51, Application US/08306691B
Patent No. 5734039
GENERAL INFORMATION:
APPLICANT: Calabretta, Bruno
APPLICANT: Skorski, Tomasz
TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306.691B
FILING DATE: September 15, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 1325 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-306-691B-51

Query Match 3.9%; Score 35.8; DB 1: Length 1325;
Best Local Similarity 48.7%; Pred. No. 0.6;
Matches 165; Conservative 0; Mismatches 162; Indels 12; Gaps 2;
OY 241 GCCCTCAATTTGAGAGGCTTGTGAAGTACACGATTTGACATTTGCTTTTCG 300
Db 322 GTGCCACCTGATGCTGGAGTCTCGAGAGACAGAAAGTGCAGAGAGGCTTCCCG 381
OY 301 TTAGCAATGAACACTTGTGATCGATTCTTATCGTTCAATGATTTGCTAGTGGCAAGGT 360
Db 382 CTGGCATTGAACACTGACCGCTTCCTGCTGAGAGCCCGT-----AAAAAG 432
OY 361 TGATATTTGACAGTTGCTGCTGTGCTTGTATTATTCATTTGACACCAAAATGAAGAACT 420

QY 241 GCCCTCAATTGATTTTGAAGCCTGTGAACATAACAAGCTTGAGCCATTGTGTTTTGC 300
QY | | | | | | | | | | | | | | | | | | | | |
Db 319 GTGGCACCTGATGTCGTGAGTCTGCCAAGAACAGAAGTCCGAGAGAGAGCTTCCCG 378
| | | | | | | | | | | | | | | | | | | | |
QY 301 TTACGATGACTACTTGATGCATGATTTATGGTTCTCATGTTGGCTAGTGGCAAGCT 360
| | | | | | | | | | | | | | | | | | | | |

Query Match	3.9%;	Score 35.8;	DB 1;	Length 4221;
Best Local Similarity	48.7%;	Pred. No. 1;		
Matches 165;	Conservative	0;	Mismatches 162;	Indels 12;
				Gaps 2;

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Query Match 3.9%: Score 35.8; DB 3; Length 4244;
Best Local Similarity 48.7%; Pred. No. 1;
Matches 165; Conservative 0; Mismatches 162; Indels 12; Gaps 2;

Qy 241 GCCCTCAATTGGATTGGAGGCTTTGTGAAGTACACAGATTGGACCAATTGTTTTC 300
Db 325 GTCCGACCTGGATGCTGAGGTCTGCCGAGAACAGAGTGGAGAGAGTCTTCCG 384
Qy 301 TTAGCAATGAACACTACTTGATGATCTTATTCGTTATGATGATTTGCTAGTGC 360
Db 385 CTGGCATTGAACACTACTTGATGATCTTATTCGTTATGATGATTTGCTAGTGC 435
Qy 361 TGGATATTGACATGTTGGCTGTGGCTTTATATCATTTGGCCGCAAAATTGAAGAA 420
Db 436 AGCCGCTGACACTGCTGGGGCCACTTGACATGTTGCTGAGCTTAAGATGAAGAGAC 494
Qy 421 GAAGTTCATGTTGATGATCTTCAAGTTGATCTTCAAGTTGATGATCTTCAAG 480
Db 495 --CATCCCCCTGACGGCCGAGAGCTGTGATCTACACCGAACAATCCATCCGCGCCGAG 552
Qy 481 TCAGTCCAAAGATGAGCTTTGTGTTGAACAAATTGAATGAGATTTGAGACAATA 540
Db 553 GAGCTGCTGCAATGAGCTGCTCTGTTGAGAACAGTCAAGTGAACCTTGCGCCGAATG 612
Qy 541 ACTCCATGCTCATACATAGATATTTCCTGAGAAAGATG 579
Db 613 ACCCGCAGATTTCATTGAAACATTCCTCTCCAAATG 651

RESULT 13

US-08-770-761A-4

Sequence 4, Application US/08770761A

Patent No. 5814503

GENERAL INFORMATION:

APPLICANT: Kovacevic, Steven

APPLICANT: Otto, Keith A.

APPLICANT: Rao, Ramachandra N.

TITLE OF INVENTION: FUSION PROTEINS COMPRISING CELL CYCLE

NUMBER OF SEQUENCES: 8

TITLE OF INVENTION: REGULATORY PROTEINS

CORRESPONDENCE ADDRESS:

ADDRESSEE: Eli Lilly and Company

STREET: Lilly Corporate Center/Patent Division

CITY: Indianapolis

STATE: IN

COUNTRY: USA

ZIP: 46285

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/770,761A

FILING DATE: 19-DEC-1996

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Gaylo, Paul J.

REGISTRATION NUMBER: 36,808

REFERENCE/DOCKET NUMBER: X-10136

TELECOMMUNICATION INFORMATION:

TELEPHONE: 317-376-0756

TELEFAX: 317-277-1917

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 4453 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-770-761A-4

Query Match 3.9%: Score 35.8; DB 1; Length 4453;
Best Local Similarity 48.7%; Pred. No. 1;
Matches 165; Conservative 0; Mismatches 162; Indels 12; Gaps 2;

Qy 241 GCCCTCAATTGGATTGGAGGCTTTGTGAAGTACACAGATTGGACCAATTGTTTTC 300
Db 253 GTCCGACCTGGATGCTGAGGTCTGCCGAGAACAGAGTGGAGAGAGTCTTCCG 2592
Qy 301 TTAGCAATGAACACTACTTGATGATCTTATTCGTTATGATGATTTGCTAGTGC 360
Db 2593 CTGGCATTGAACACTACTTGATGATCTTATTCGTTATGATGATTTGCTAGTGC 2643
Qy 361 TGGATATTGACATGTTGGCTGTGGCTTTATATCATTTGGCCGCAAAATTGAAGAA 420
Db 2644 AGCCGCTGACACTGCTGGGGCCACTTGACATGTTGCTGAGCTTAAGATGAAGAGAC 2702
Qy 421 GAAGTTCATGTTGATGATCTTCAAGTTGATCTTCAAGTTGATGATCTTCAAG 480
Db 2703 --CATCCCCCTGACGGCCGAGAGCTGTGATCTACACCGAACAATCCATCCGCGCCGAG 2760
Qy 481 TCAGTCCAAAGATGAGCTTTGTGTTGAACAAATTGAATGAGATTTGAGACAATA 540
Db 2761 GAGCTGCTGCAATGAGCTGCTCTGTTGAGAACAGTCAAGTGAACCTTGCGCCGAATG 2820
Qy 541 ACTCCATGCTCATACATAGATATTTCCTGAGAAAGATG 579
Db 2821 ACCCGCAGATTTCATTGAAACATTCCTCTCCAAATG 2859

RESULT 14

US-08-770-761A-6

Sequence 6, Application US/08770761A

Patent No. 5814503

GENERAL INFORMATION:

APPLICANT: Kovacevic, Steven

APPLICANT: Otto, Keith A.

APPLICANT: Rao, Ramachandra N.

TITLE OF INVENTION: FUSION PROTEINS COMPRISING CELL CYCLE

NUMBER OF SEQUENCES: 8

TITLE OF INVENTION: REGULATORY PROTEINS

CORRESPONDENCE ADDRESS:

ADDRESSEE: Eli Lilly and Company

STREET: Lilly Corporate Center/Patent Division

CITY: Indianapolis

STATE: IN

COUNTRY: USA

ZIP: 46285

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/770,761A

FILING DATE: 19-DEC-1996

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Gaylo, Paul J.

REGISTRATION NUMBER: 36,808

REFERENCE/DOCKET NUMBER: X-10136

TELECOMMUNICATION INFORMATION:

TELEPHONE: 317-376-0756

TELEFAX: 317-277-1917

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 4540 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-770-761A-6

Query Match 3.9%; Score 35.8; DB 1; Length 4540;
 Best Local Similarity 48.7%; Pred. No. 1.1;
 Matches 165; Conservative 0; Mismatches 162; Indels 12; Gaps 2;

OY 241 GCCCCTCAATGGATTGGAGGCTGTGTAAGTACACAGTTTGGACCATTTGTTTTC 300
 DB 2533 GTCCGCACCTGGATGCTGGAGGCTGTGCGAGCAAGAAATGGAGAGAGGCTTCCCG 2592
 OY 301 TTAGCAATGAACTACTTGGATGATCTTATGCTTTCATGATTTGCTTGAAGAGT 360
 DB 2593 CTGGCCATGAATACCTGGAGCCGCTTCTGCTGGAGACCCGCTG-----AAAAG 2643
 OY 361 TGGATATTGCACTGTGTGCTGTGGCTTTATCATTTGGCAGCCAAATTTGAAGAACT 420
 DB 2644 ACCCGCTGCACTGTGTGGGCGCACTTGCATGTCGCTTAAGATGAAGAGAGAC- 2702
 OY 421 GAAGTTCCAAATGTTAGATCTTCAGTTTGAAGATCTCAGTTTGTGTTGAGGCTTAA 480
 DB 2703 --CATCCCTTACGCGCCGAGAAAGCTGTGCATCTACCGACAACCTCCATCCGCGCGAG 2760
 OY 481 TCAGTCCAAAGATGAGCTTTTGTGTGTAACAAATTTGAATGAGATTTGAGAGCAATA 540
 DB 2761 GAGCTGCTCAATGAGAGCTGCTCTGCTGTGAACAAGCTCAAGTGAAGCACTGGCGCGAATG 2820
 OY 541 ACTCCATGCTCATACATAAGATATTTCCTGAGAAAGATG 579
 DB 2821 ACCCGCAGATTTCAATGAACACTTCCTCCAAATG 2859

RESULT 15
 US-08-770-761A-1
 ; Sequence 1, Application US/08770761A
 ; Patent No. 5814503
 ; GENERAL INFORMATION:
 ; APPLICANT: Kovacevic, Steven
 ; APPLICANT: Rao, Ramachandra N.
 ; TITLE OF INVENTION: FUSION PROTEINS COMPRISING CELL CYCLE
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Eli Lilly and Company
 ; STREET: Lilly Corporate Center/Patent Division
 ; CITY: Indianapolis
 ; STATE: IN
 ; COUNTRY: USA
 ; ZIP: 46285
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/770,761A
 ; FILING DATE: 19-DEC-1996
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Gaylo, Paul J.
 ; REGISTRATION NUMBER: 36,808
 ; REFERENCE/DOCKET NUMBER: X-10136
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 317-376-0756
 ; TELEFAX: 317-277-1917
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4621 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-08-770-761A-1

Query Match 3.9%; Score 35.8; DB 1; Length 4621;
 Best Local Similarity 48.7%; Pred. No. 1.1;
 Matches 165; Conservative 0; Mismatches 162; Indels 12; Gaps 2;

OY 241 GCCCCTCAATGGATTGGAGGCTGTGTAAGTACACAGTTTGGACCATTTGTTTTC 300
 DB 2484 GTCCGCACCTGGATGCTGGAGGCTGTGCGAGCAAGAAATGGAGAGAGGCTTCCCG 2543
 OY 301 TTAGCAATGAACTACTTGGATGATCTTATGCTTTCATGATTTGCTTGAAGAGT 360
 DB 2544 CTGGCCATGAATACCTGGAGCCGCTTCTGCTGGAGACCCGCTG-----AAAAG 2594
 OY 361 TGGATATTGCACTGTGTGCTGTGGCTTTATCATTTGGCAGCCAAATTTGAAGAACT 420
 DB 2595 ACCCGCTGCACTGTGTGGGCGCACTTGCATGTCGCTTAAGATGAAGAGAGAC- 2653
 OY 421 GAAGTTCCAAATGTTAGATCTTCAGTTTGAAGATCTCAGTTTGTGTTGAGGCTTAA 480
 DB 2654 --CATCCCTTACGCGCCGAGAAAGCTGTGCATCTACCGACAACCTCCATCCGCGCGAG 2711
 OY 481 TCAGTCCAAAGATGAGCTTTTGTGTGTAACAAATTTGAATGAGATTTGAGAGCAATA 540
 DB 2712 GAGCTGCTCAATGAGAGCTGCTCTGCTGTGAACAAGCTCAAGTGAAGCACTGGCGCGAATG 2771
 OY 541 ACTCCATGCTCATACATAAGATATTTCCTGAGAAAGATG 579
 DB 2772 ACCCGCAGATTTCAATGAACACTTCCTCCAAATG 2810

Search completed: January 21, 2002, 00:20:01
 Job time: 2935 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 20, 2002, 22:59:31 ; Search time 1163.67 Seconds

(without alignments)
8560.276 Million cell updates/sec

Title: US-09-530-209A-1

Perfect score: 927
Sequence: 1 ATGCGACGAGGAAATCTAGA.....CTTATACATCTTCTTA 927

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : 1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_htc:*
10: qd_est1:*
11: qd_est2:*
12: qd_htc:*
13: qb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rtd:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	264.6	28.5	673	11	BG129531 EST475177
2	202.4	21.8	631	10	AM507921 s147a06.y
3	169.2	18.3	512	10	AT1728767 BNLGH1115
4	163.4	17.6	790	11	BI306295 NL_4_B12
5	153	16.5	562	10	AT1728683 BNLGH1113
6	149.2	16.1	621	13	CNS00055 Arabidops
7	149.2	16.1	621	10	BE442681 WHE1101_A
8	123.6	13.3	813	10	BE642779 Cri12_6_P2
9	116	12.5	478	10	AV527915 AV527915
10	111.8	12.1	596	10	AM042725 ST24F07_P
11	111.6	12.0	498	11	BG726093 sae06h09.
12	110.6	11.9	558	10	AM036252 EST278331

13	109.8	11.8	775	11	BG645553
14	109.8	11.8	809	11	BG585146
15	109.2	11.8	810	11	BG646052
16	107.6	11.6	834	11	BG585934
17	107.4	11.6	583	10	A1812774 18H7 pine
18	104.6	11.3	749	11	BG886881
19	103	11.1	728	11	BG597062
20	102.6	11.1	666	11	B1210187
21	101	10.9	608	10	AM735876
22	101	10.9	802	11	B1207010
23	100	10.8	768	11	BG643290
24	99.2	10.7	805	10	AT1725905
25	98.2	10.6	717	10	AM623899
26	97	10.5	450	11	B1204344
27	97	10.5	516	11	B1211043
28	97	10.5	546	11	B1204893
29	97	10.5	725	11	B1203937
30	97	10.5	727	11	B1204715
31	97	10.5	727	11	B1205090
32	96	10.4	487	11	BF096480
33	95	10.2	785	11	B1206688
34	93.6	10.1	840	11	BF272373
35	92.8	10.0	592	10	AM934320
36	92.4	10.0	663	11	B1270081
37	92.2	9.9	742	11	BG125807
38	91.2	9.8	565	11	B1140861
39	88.6	9.6	423	10	AM278395
40	87.8	9.5	625	13	AO842192
41	86.8	9.4	486	10	BE499582
42	86.6	9.3	569	11	B1076149
43	85.4	9.2	613	10	BE511087
44	84.8	9.1	778	11	BG128733
45	84.2	9.1	587	13	B24616

ALIGNMENTS

RESULT 1	BG129531	673 bp	EST	31-JAN-2001
LOCUS	EST475177	tomato shoot/meristem	Lycopersicon esculentum	CDNA clone
DEFINITION	CTOP24H8 5' sequence, mRNA sequence.			
ACCESSION	BG129531			
VERSION	BG129531.1	GI:12629719		
KEYWORDS	EST.			
SOURCE	tomato.			
ORGANISM	Lycopersicon esculentum			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
	Asteridae; euasterids I; Solanales; Solanaceae; Solanum;			
	Lycopersicon.			
REFERENCE	1 (bases 1 to 673)			
AUTHORS	van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Uterback,T.,			
	Hansen,C., Ronning,C. and Tankley,S.			
TITLE	Generation of ESTs from tomato shoot/meristem tissue			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: CGI			
	Clemson University Genomics Institute			
	Clemson University			
	100 Jordan Hall, Clemson, SC 29634, USA			
	Email: http://www.genome.clemson.edu/orders/index.html .			
FEATURES	location/Qualifiers			
source	1..673			
	/organism="Lycopersicon esculentum"			
	/cultivar="FA496"			
	/db_xref="taxon:4081"			
	/clone="CTOP24H8"			
	/clone_lib="tomato shoot/meristem"			
	/rissue_type="shoot/meristem"			
	/dev_stage="developing shoots from 4-6wks old plants"			
	/lab_host="SOLR"			
	/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:			

OY	662	TTTTGGACCTTAGACCTTCTGAAGCTGCTGTCTGTGGACACTTTTCGTTCTTGAGAAT	721
DB	366	TCTTGCATTATTAACCCATCAGCATGATTTGACGACGACGATGCGTATGATGATTCATGAGGGAA	425
OY	722	TGCAAGAGTACACTTTTACACACTCTTCCTCTCTCCCTTTTCTCACACTTCAAAAG	781
DB	426	CCCCAACAGCTTGACCTGGAA---AGCAATCTCTGTTCTGATTCACACGTGAATAGG	482
OY	782	AGAGAGTGAAGATATGAGGAAATGAT	809
DB	483	AGAGACTATTGTAAGTGTGTTCAAATGAT	510
RESULT	3		
LOCUS	A1728767	512 bp	mRNA EST 11-JUN-1999
DEFINITION	BNGH11561 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (A011892) cyclin D2.1 protein [Nicotiana tabacum], mRNA sequence.		
ACCESSION	A1728767		
VERSION	A1728767.1	GI:5047619	
KEYWORDS	EST.		
SOURCE	upland cotton.		
ORGANISM	Gossypium hirsutum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium. Blewitt, M., Matz, E.C., Davy, D.F. and Burr, B. ESTs from developing cotton fiber Unpublished (1999)		
AUTHORS	Contact: Ben Burr		
JOURNAL	Biology Department		
COMMENT	Brookhaven National Laboratory Upton, NY 11973, USA Tel.: 516-344-3396 Fax: 516-344-3407 Email: burr@nsluxl.bnl.gov Seq primer: 73 primer.		
FEATURES	Location/Qualifiers		
SOURCE	1. 512		
	/organism="Gossypium hirsutum"		
	/cultivar="Acala Maxxa"		
	/db_xref="taxon:3635"		
	/clone_lib="Six-day Cotton fiber"		
	/tissue_type="Immature fiber"		
	/dev_stage="Six days post anthesis"		
	/lab_host="XL1-Blue"		
	/note="Vector: pBluescript II KS+"		
BASE COUNT	146 a 86 c 113 g 167 t		
ORIGIN			
Query Match	18.3%; Score 169.2; DB 10; Length 512;		
Best Local Similarity	74.8%; Pred. No. 2.1e-33;		
Matches 226; Conservative	0; Mismatches 73; Indels 3; Gaps 1.		
OY	125	AGAGTGAGAGATTTCATGAGATGCTGTGGACAAGAGACAGCATTTGCCAAGTGATG	184
DB	214	AAAAGTGATGATGAAATCAAAAGAGATGTTGAANAAGAGGTGAGCATTTGCCGTAAGAG	273
OY	185	ATTATATCAAGAGACTTTGAAGTGAAGATTTGAAATGTTGGAAGAGATGCGCC	244
DB	274	ATTATCTCAAGAGACTGACAAAGTGGGATTTGACTTGAGTGT---ACGAAGAAGGCTC	330
OY	245	TCAATTGATTTGGAAGGCTTGTAAGTACACACAGTTGGACATTTGCTTTTGCTTAG	304
DB	331	TTCATTGATTTGGAAGGCTTCTGCTTATTAAGTTTGGACCTTTGATCTTTGGCTAT	390
OY	305	CATGACACTCTTGATGATTCATTCGCTTCATGATTTGGCTCTGATGGCAAAAGTTGCA	364

QY	DB	365	TATTCGACGTTGTTGGCTGTGCGCTTGTATATCATTCGACACCAAAATGGAAGAACTGAAG	424
DB	451	CCGTCACATTCGCTTCGTCTGCTTATATCAATTCGACCAAAATGAGAGACAAAG	510	
QY	425	TT 426		
DB	511	TT 512		
RESULT	4			
LOCUS	BI306295/c			
DEFINITION	BI306295	790 bp	mRNA	EST
ACCESSION	BI306295			20-JUL-2001
KEYWORDS	EST			
SOURCE	ORYZA SATIVA			
ORGANISM	ORYZA SATIVA			
REFERENCE	Reddy, A.R., Kamakrishna, W., Chandrasekhar, A., Nagabhusan, I., Ravindrababu, P., and Bennetzen, J.L.			
AUTHORS	Novel EST enrichment with normalized cDNA libraries from drought stressed rice (Oryza sativa L. cv Nagina 22)			
TITLE	Unpublished (2001)			
JOURNAL	Contact: Reddy AR			
COMMENT	Department of Plant Sciences, School of Life Sciences University of Hyderabad P.O. Central University, Hyderabad-500 046, A.P., India Tel: 0091-40-3010265 Fax: 0091-40-3010145 Email: arjuls@uohyd.ernet.in Insert Length: 790 Std Error: 0.00 Plate: 4 Row: B Column: 12 Seq primer: GTAAACGACGCGCAGTCG.			
FEATURES	Location/Qualifiers			
SOURCE	1..790			
	/organism="Oryza sativa"			
	/cultivar="Nagina 22 (Indica sub sp)"			
	/db_xref="taxon:4530"			
	/clone="NL_4_B12"			
	/clone_lib="Drought stress (leaf)"			
	/tissue_type="Entire leaf tissue"			
	/dev_stage="35 day-old seedlings"			
	/note="Organ: Leaf; Vector: pTZ19pac; ESTs from normalized leaf cDNA library from drought stressed seedlings"			
BASE COUNT	222 a	239 c	179 g	150 t
ORIGIN				
Query Match	17.6%	Score 163.4;	DB 11;	Length 790;
Best Local Similarity	58.7%;	Pred. No. 7.3e-32;		
Matches 322;	Conservative	0;	Mismatches 221;	Indels 6;
			Gaps	2
QY	130	GAGGAGATTATCATGAGATGTTGGAAGAGGAGAACACATTTGCCAAGTATGATTAC	189	
DB	590	GATGAGTTCTGTGCGCTTGTGTTGGTGGAAGAGATGATCATCAGCCTCAGCGGGGTAT	531	
QY	190	ATCAGAGACCTTAAAGATGAGATTTGATTTGAATGTTGGAAGAGATGCCCTCAT	249	
DB	530	CTGGAGAACTGGAGCTCGGTGATTGGA---GTGTTCTTGGAGAAATGCAATTCAT	474	
QY	250	TGATTTGGAAGGCTTGTGAAGTACACCGATTTGGACATTTGTTGTTGCTTAGCAATG	309	
DB	473	TGATTTTCCAAAGCTCCATTCCTACACAACTTTGGACCACTCAGCCTTACCTCGCAGTG	414	
QY	310	AACACTTGATGATTTCTTATCGGTTCAATGATTTGCCCTAGTGGCAAGCTTGATATTG	369	

```

Db 413 AACTAACGTGATAGAGTTCCTCCCTCCGTTTAATCTCCATGACGACATCTTGATGCAA 354
QY 370 CAGTTGTTGGCTGTGGCTTGTATTATCATTTGGACGCCAAATTTGAGAATCTGAGTTCCA 429
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 353 CAGTTGCTGTCAAGTATGTTGCTATCTCTTGTACGAATGAGAGAGACCGGTGCTCC 294
QY 430 AAGTTGATGATCTTCAGTTGGAGATCCTCAGTTGGTGGAGCTTAATGAGCCAA 489
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 293 CTTCCATGAGCTTCAGTTGTTTGTGGGGAATATGATTTTGAACCAAGGCAATTAAG 234
QY 490 AGAATGAGCTTTTGTGTTTGAACAATTTGAATGAGATTTGAGACCAATTAATCCATGC 549
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 233 AGGATGAGACTTATTTGTATGAAACCCGTAATGAGAGCTGCAACCTGACCCCATTC 174
QY 550 TCATACATAGATATTTCTCTGAGAAAGATGAGTAATTTGATCAGAACCATCCAAACA 609
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 173 TCTTTTCATCGGCTACTTCTCGACAACTTCAATGAGGAGAGC---CGCGAGCTTCACAG 117
QY 610 TTGATATCTAGATCAATTAAGATGACGACACAAACCAAGGTAATGACTTTTGGAG 669
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 116 CTGGCATCTAGTGTCTGATCTCACAGTGGCAGCTTGAAAGACTTGAAGTTCTTGTA 57
QY 670 TTTAGACT 678
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 56 TTCAGACT 48

RESULT 5
A1728683 562 bp mRNA EST 11-JUN-1999
LOCUS BN1GH11316 six-day cotton fiber Gossypium hirsutum cDNA 5' similar
DEFINITION to (A0101892) cyclin D2.1 protein [Nicotiana tabacum], mRNA
sequence.
ACCESSION A1728683
VERSION A1728683.1 GI:5047535
KEYWORDS EST.
SOURCE upland cotton.
ORGANISM Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
REFERENCE 1 (bases 1 to 562)
AUTHORS Blewitt,M., Matz,E.C., Davy,D.F. and Burr,B.
TITLE ESTs from developing cotton fiber
JOURNAL Unpublished (1999)
COMMENT Contact: Ben Burr
Biology Department
Brookhaven National Laboratory
Upton, NY 11973, USA
Tel: 516-344-3396
Fax: 516-344-3407
Email: burr@bnl1.bnl.gov
Seq primer: T3 Primer.
FEATURES
    source
        1..562
            /organism="Gossypium hirsutum"
            /cultivar="Acala Maxxa"
            /db_xref="taxon:3635"
            /clone_lib="Six-day Cotton fiber"
            /tissue_type="Immature fiber"
            /dev_stage="Six days post anthesis"
            /lab_host="XL1-Blue"
            /note="Vector: pBluescript II KS+"
BASE COUNT 156 a 101 c 117 g 186 t 2 others
ORIGIN
Query Match 16.5%; Score 153; DB 10; Length 562;
Best Local Similarity 69.8%; Pred. No. 3.4e-29;
Matches 220; Conservative 0; Mismatches 92; Indels 3; Gaps 1;
QY 114 TTCTCAATCGAGAGTGAAGATTTATCATGAGATGTTGGAAGAGAGAGCAGCATTT 173
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 244 TTTTCATTACAAAGCATGATGATTAATTAAGCAATGTTGAAGAGATGAGCATTT 303
QY 174 GCCAGTGTATGATTACATACAGACTTGAAGTGAAGATTGGATTGAATTTGAAG 233
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 304 GCCATAGATGATTAATCTTAAGAGACTGAGAACTGGGGATTGGAGTTGA---GCGCCAC 360
QY 234 AAGAGATGCCCAATTTGATTTGGAAGCTTGAAGTACACACACTTTGGACATTTG 293
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 GAGAGAGCTTAATGAATGATTTGGAAGGCTTCANCTTAATTTCAATTTGGAGCTTGAG 420
QY 294 TTTTTCCTTACGAATGAACTACTTGGATGATCTTATGCGTTTCATGATTTGGCTAGTG 353
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 421 TCTTTCCATATCATTAATCACTGATGATGCTTCATCAATATGATTAATTAACCTAGAG 480
QY 354 CAAAGTTGATATTTGCACTTGTGCTGTGCTTTTATCATTTGGACGCCAAATTTGA 413
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 TAAACATGAGACTTCACAACTGTGGCCGTGATGTTATTAATTCANCTAATAATGTA 540
QY 414 AGAAGTGAAGTTCC 428
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 GGAACCAAGGTGCC 555

RESULT 6
CNS00055 381 bp DNA GSS 28-JUN-1999
LOCUS CNS00055
DEFINITION Arabidopsis thaliana genome survey sequence Sp6 end of BAC T8D11 of
TAMU library from strain Columbia of Arabidopsis thaliana, genomic
survey sequence.
ACCESSION AL090574
VERSION AL090574.1 GI:5291714
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 381)
AUTHORS Salanoubat,M., Choise,N., Arisgouane,F., Brotier,P., Wincker,P.,
Samson,D., Saurin,W., Weissenbach,J. and Quetier,F.
JOURNAL Unpublished
TITLE 2 (bases 1 to 381)
AUTHORS Genoscope.
JOURNAL Direct Submission
Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
FEATURES
    source
        1..381
            /organism="Arabidopsis thaliana"
            /strain="Columbia"
            /db_xref="taxon:3702"
            /clone_lib="TAMU"
            /clone="T8D11"
            /note="end : SP6"
BASE COUNT 140 a 42 c 69 g 130 t
ORIGIN
Query Match 16.1%; Score 149.2; DB 13; Length 381;
Best Local Similarity 92.4%; Pred. No. 3e-28;
Matches 157; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 758 CTTCTTTCACACTACTTCAAGAGAGAGTGAAGAAGATAGGGGAAATGATAGAGAGTG 817
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5 CTTTGTGTTCTTTTATTGACAGAGAGTGAAGAAGATAGGGGAAATGATAGAGAGTG 64
QY 818 ATGGCTCAGACTATATGTGCAAAACCAATGCGGTTTGAAGATGCGCTTGTGTT 877
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 65 ATGGCTCAGACTATATGTGCAAAACCAATGCGGTTTGAAGATGCGCTTGTGTT 124
QY 878 TTAGCTTAAGACCAATGATTTCTTCTTCTTATACACATCTTCTTAA 927
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Best Local Similarity 62.4%; Pred. No. 1.6e-21;
Matches 211; Conservative 0; Mismatches 124; Indels 3; Gaps 1;

QY 241 GCCCTCAATTGGATTGGGAAGCCTTGAAGTACACCATTTGGACCATTTGCTTTTTCG 300
 Db 19 GCATATGAGCTGATTTCTAAGTTCAGAGATTCACAAATTTGGCCTTGGATGCGC 78
 QY 301 TTGCAATGACATCTGATGATCTTATCGCTTCAATGATTTGGCTAGTGGCAAGGT 360
 Db 79 CTCTGTGAGTACGCTGATGATCTTCTTCTGTCAAAAGATCCGGCTGGAAACCG 138
 QY 361 TGGATTTGAGCTTTGCTGCTTGTGCTTTTATTCATTTGGCAGCCAAATTTGAAGAACT 420
 Db 139 TGGATATGACATGCTGATGCTGATGCTGATGCTGATGCTGCTGCTGCTGCTGCTG 198
 QY 421 GAAGTTCATTTGATAGATCTTCAAGCTTTGGAGATCTTCTGCTTGTGAGGCTAAA 480
 Db 199 GAGGTCCGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 255
 QY 481 TCAGTCCAAAGATGAGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
 Db 256 ACATTCACATGATGAGTACTTGTGCTGAGCAGCTTGAATGGCAATGAGTCTTGTG 315
 QY 541 ACTCATGCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 578
 Db 316 ACACCATTTGCTTATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 353

RESULT 9

AV527915 478 bp mRNA EST 01-SEP-2000
 LOCUS AV527915 Arabidopsis thaliana aboveground organs two to six-week
 DEFINITION old Arabidopsis thaliana cDNA clone AP247c12R 5', mRNA sequence.
 ACCESSION AV527915
 VERSION AV527915.1 GI:8687443
 KEYWORDS EST.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana

REFERENCE
 AUTHORS Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
 TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation
 of 12,028 non-redundant expressed sequence tags from normalized and
 size selected cDNA libraries
 JOURNAL DNA Res. 7, 175-180 (2000)
 COMMENT Contact: Erika Asamizu
 MEDLINE 20363093
 The First Laboratory for Plant Gene Research
 Kazusa DNA Research Institute
 Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
 Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/
 Location/Qualifiers

FEATURES
 source
 1..478
 /organism="Arabidopsis thaliana"
 /strain="Columbia"
 /db_xref="taxon:3702"
 /clone="AP247c12R"
 /clone_lib="Arabidopsis thaliana aboveground organs two to
 six-week old"
 /tissue_type="aboveground organs"
 /dev_stage="two to six-week old"
 /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
 XhoI"

BASE COUNT 125 a 86 c 105 g 162 t
 ORIGIN

Query Match 12.5%; Score 116; DB 10; Length 478;
 Best Local Similarity 58.3%; Pred. No. 1.3e-19;
 Matches 203; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

QY 210 AGATTGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 269
 Db 49 AGATGCTTTTGTGCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 108
 QY 270 AGTACACAGATTTGGACCATTTGTTTGTGCTTGGCAATGAACTACTTGATGATCTT 329
 Db 109 TCATTATGAGTTTACTTCAATGACGCTATACTTGTGCTGCACTACTGATGATGATG 168
 QY 330 ATCGTTTCATGATTTGCTCTAGTGGCAAGGTGGATATTCAGTCTTGTGCTGCTT 389
 Db 169 GACAAAGTATTAACCTTCACTGCTGATGATGATGATGATGATGATGATGATGATG 228
 QY 390 TTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 449
 Db 229 TTTGCTTTTACGCTGCTTAAAGTTCAAGATTTCAAGTTCCATTTCTTACCTCCAA 288
 QY 450 TGGAGTCTCTCACTTTGTGTTGAGGCTTAATCAGTCCAAAGATGAGCTTTGCTGTT 509
 Db 289 GGAAGAAGCAAGATATCTCTTTGAGCTAAGAGATTCAAAGATGAGAGCTTTGATTC 348
 QY 510 GAACAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 557
 Db 349 TTCTACTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 396

RESULT 10

AW042725 596 bp mRNA EST 18-SEP-1999
 LOCUS ST24F07 Pine Triplex shoot tip library Pinus taeda cDNA clone
 DEFINITION ST24F07, mRNA sequence.
 ACCESSION AW042725
 VERSION AW042725.1 GI:5903254
 KEYWORDS EST.
 SOURCE loblolly pine.
 ORGANISM Pinus taeda

REFERENCE
 AUTHORS Whetten, R.W., Kinlaw, C.S., Retzel, E. and Sederoff, R.R.
 TITLE The Pine Gene Discovery Project
 JOURNAL Unpublished (1999)
 COMMENT Contact: Ross Whetten
 Forest Biotechnology Group
 North Carolina State University
 Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh
 NC, 27695-8008
 Tel: 919-515-7800
 Fax: 919-515-7801
 Email: rosswhetten@unity.ncsu.edu
 Seq primer: 5' lambda Triplex2 sequencing primer.
 Location/Qualifiers

FEATURES
 source
 1..596
 /organism="Pinus taeda"
 /db_xref="taxon:3352"
 /clone="ST24F07"
 /clone_lib="Pine Triplex shoot tip library"
 /lab_host="E. coli BM25.8"
 /note="Organ: shoot tips; Vector: Lambda Triplex; Site_1:
 SfiI (A); Site_2: SfiI (B); Shoot tips (approx. 2 cm from
 apex) were collected during the spring, frozen and used
 for mRNA isolation. The SMART-PCR method (Clontech) was
 used to prepare a library from 1 ug total RNA, using the
 Lambda Triplex vector. Plasmid subclones in pTriplex were
 recovered by cre-lox excision in E. coli strain BM25.8 and
 sequenced from the 5' end."

BASE COUNT 135 a 152 c 153 g 151 t 5 others
 ORIGIN

Query Match 12.1%; Score 111.8; DB 10; Length 596;
 Best Local Similarity 56.3%; Pred. No. 1.7e-18;
 Matches 228; Conservative 0; Mismatches 174; Indels 3; Gaps 1;


```
/organism="Lycopersicon esculentum"
/cultivar="RA496"
/db_xref="taxon:4081"
/clone="cLEED20"
/clone_lib="Tomato seed, TAMU"
```

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/lissue_type="seeds"
/dev_stage="quiescent seed"
/lab_host="XLI-Blue MRF"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; cLEE - Tomato Seed EST Library. Directionally cloned
cDNAs inserted into pBluescript SK(-) at 5' end with
EcoRI and 3' end with XhoI site."

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BASE COUNT      149 a      97 c      111 g      201 t
ORIGIN
Query Match      11.9%; Score 110.6; DB 10; Length 558;
Best Local Similarity 57.8%; Pred. No. 3.5e-18;
Matches 197; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

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QY 238 GATGCCCTCAATTGGATTGGGAAGCGTTGTGAAGTACACCAGTTGGACCATTTGTGTTT 237
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 149 GATGTTGTTGAAATGATCTTAAAGTAAGTCAATTAATGATTCAGCATTTGACTGCC 208
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 298 TGGTATGCAATGACTACTGATGATTCCTTATCGGTTTCATGATTTGCCATGCGCAA 357
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 209 ATTTTGGCCATTATATCTTGACAGGTTCTTTAGCCTTAATTTTCAGAAAGATAAG 268
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 358 GGTGGATATTTGCAATGTTGGCTGTGCTGCTTTATTCATTTGGCAGCCAAATTTGAAGA 417
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 269 CCATGGATGATCACTACACTGTGCTGCTGCTCTTCTTTAGCGGCTAAAGTTGAAGA 328
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 418 ACTGAAGTTCCAAATGTTGATAGATCTTCAGAGTTGGAGATCTCAGTTTGTGAGGCT 477
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 329 ACTCAAGTTCCCTTCTTCTTGACTTCCAAAGTGAAGATGCAAAATATGTTGTTGAGGCA 388
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 478 AATTCATGCAAGTAAGTGAAGCTTTGGTGTGTAACAATTTGAATGGAATGAGAGCA 537
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 389 AATGATATCAAAAGTAAGGAGCTTGTGACTCTCATCACTGAAATGAGAGATATCCA 448
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 538 ATACTCTCATGCTCATATCAATAGATATTTCTTGAGAAAGAT 578
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 449 GTGACCCCACTTTCATTTCTTGATCATATATTAAGAAAGCT 489
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 13
LOCUS      BG645553      775 bp      mRNA      EST      24-APR-2001
DEFINITION EST071172 KV3 Medicago truncatula cDNA clone pKV3-46J23 5' end,
            mRNA sequence.
ACCESSION  BG645553
VERSION     BG645553.1 GI:13780665
KEYWORDS    EST.
SOURCE      barrel medic.
ORGANISM    Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
            Medicago.
            1 (bases 1 to 775)

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REFERENCE  1 (bases 1 to 775)
AUTHORS    Vandenbosch, K., Endre, G., Hur, J., Beremand, P., Town, C.D., Bowman
            , C.L., Craven, M.B., Cho, J. and Fraser, C.M.
TITLE       ESTs from roots of Medicago truncatula 72 h after Rhizobium
            inoculation, 2001
JOURNAL     Unpublished (2001)
COMMENT     Contact: Vandenbosch K
            Department of Biology
            Texas A&M University
            College Station, TX 77843-3258, USA
            Tel: 409 845 7707
            Fax: 409 845 2891
            Email: kate@mail.bio.tamu.edu
            M3939606 TIGR sequence name: MTECC607K More information is
            available at: www.medicago.org
            Seg primer: SKmod (CTA GAA CTA 9tg gat CC).
            Location/Qualifiers
            1..775
            /organism="Medicago truncatula"

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FEATURES
source
1..775
/organism="Medicago truncatula"

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/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pKV3-46J23"
/clone_1lb="KV3"
/lissue_type="Seedling roots"
/dev_stage="3 days post-inoculation with Sinorhizobium
meliloti"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the UniZap XR vector from
Stratagene and packaged using GigaPack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-zap phage using Ex-assist
helper phage and propagated in XL04R cells."

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BASE COUNT      183 a      185 c      167 g      240 t
ORIGIN
Query Match      11.8%; Score 109.8; DB 11; Length 775;
Best Local Similarity 50.7%; Pred. No. 6.1e-18;
Matches 317; Conservative 0; Mismatches 302; Indels 6; Gaps 2;

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QY 123 GGAGAGTGAAGATTTATCATGAGATGTGTGAAGAGAACACCAATTTGCCAAGTGA 182
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 127 GGAAGAGAGAGATGCATGCTGTTTTCATCGACAGCAAGTTCAAGTTGTTCTGTTT 186
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 183 TGATTCATCAACAGACTTAGAAGTGAAGTGGAGATTTGATTTGAATGTTGGAAGAAGATGC 242
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 187 CGACTACGTCATCAAGATTCCTCAATCTGCTCTCGAATCCA--GCACAGAGAGAAAGC 243
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 243 CCTCATTTGGATTTGGAAGGCTTGTGAAGTACACAGTTTGGACCAATTTGTTTGGCTT 302
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 244 CATTGCATGGAATTCGACGATACATGATATATGATATGATTTGATTTGACGCTTAACGCGTAC 303
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 303 AGCAATGACTACTTGTGATGATCTTATTCGATTCATGATTTGCTTATGTCGAAGGTTG 362
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 304 CTCCGTTAATATATGATGATGCTGTTTGGATTCGACCTTTACGGAAATCAATATGATG 363
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 363 GATATTTGACAGTTGTGCTGTGCTGCTTTATCATTTGATTTGATTTGATTTGATTTGATTT 422
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 364 GCCACTGCAACTTTATCTGCTGATGTTTGTCTTATGAGCAAGAAATGAGAGACCACT 423
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 423 AGTTCAATTTGATGATCTTCAGTGTGAGATGCTCAGTTTGTGTTGAGGCTTAATC 482
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 424 GGTTCCTTCTCTTGAAGCTTGTGATTTGAAGTGTCCAAATATCATTTTCAACCAAGAC 483
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 483 AGTCAAGATGAGACTTTTGTGTTGAACAATTTGAATGAGATTTGAGACCAATATAC 542
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 484 GATTTCTTAGATGAGCTGTTGTTGACTATTTTGAATTTGAGAGGCTGAGATCAATCAC 543
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 543 TCCATCTCTACATATAGATATTTCTTGAGAAAGATGAGTAAATTTGATTCAGAACATC 602
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 544 CCCACTTAGTTCCCTCAGATTTCTTTCGCAAGCTAGATTCACATG---GAACCTTTCAC 600
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 603 CACACATTTGATTTATGATCATTTACAGATGATGAGCAGCAGCAACCAAGATTTGACTT 662
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 601 CCATTCATATTTTCAAGCTGCTACAGAAATCAATCTTATATATCAAGATCTTACTT 660
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 663 TTTGAGATTTAGACTTTGAGAGCTGCTGCTGCTGAGCACTTTGTTTGTGAGAAAT 722
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 661 TCTTACTTACAGGCATCATGATTTGCTGAGCTGCGCATATCTCTGACGATATGAAT 720
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 723 GCAGAGATGACTTTGACAACTCT 747
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 721 TCTTAATGTGCTTTTGTAAATCTT 745
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 14
LOCUS      BG585146      809 bp      mRNA      EST      11-APR-2001
DEFINITION EST486909 MHAM Medicago truncatula/Gliomus versiforme mixed EST
            library cDNA clone pMHAM-22A23 5' end, mRNA sequence.

```

ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
BC585146	1	GI:13600210							
EST									
Medicago truncatula/Glomus versiforme mixed EST library.									
Medicago truncatula/Glomus versiforme mixed EST library									
Eukaryota: mixed EST libraries.									
1 (bases 1 to 809)									
Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Uterback,T., Cho,J.									
and Fraser,C.M.									
ESTs from roots of Medicago truncatula after colonization with									
Glomus versiforme, 2001									
Unpublished (2001)									
Contact: Harrison M.J.									
Plant Biology Division									
The Samuel Roberts Noble Foundation									
2510 Sam Noble Parkway, Ardmore, OK 73401									
Tel: 580-223-5810									
Fax: 580-221-7380									
Email: mjharrison@noble.org									
Noble EST name: N380619e TIGR sequence name: MTDCAL2TK More									
information is available at: http://www.medicago.org									
Seq primer: SKmod (CTA GAA CTA gfg gAT CC).									
Location/Qualifiers									
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/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days									
post-inoculation with Glomus versiforme. The library was									
made from a mixture of RNA from each of these stages."									
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/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:									
XhoI; CDNA was prepared from polyA+ enriched RNA from									
roots harvested at 10, 17, 22, 31 and 38 days									
post-inoculation with Glomus versiforme. The CDNA was									
directionally ligated into the UniZap XR vector from									
Stratagene and packaged using GigaPack III Gold packaging									
extracts. Plasmids containing CDNA inserts were excised									
from the recombinant lambda-Zap phage using Ex-assist									
helper phage and propagated in XL0LR cells."									
BASE COUNT	194 a	196 c	173 g	246 t					
ORIGIN									
Query Match	11.8%	Score 109.8	DB 11	Length 809					
Best Local Similarity	50.7%	Pred. No. 6.1e-18							
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213	CGACGACGCTCAAGATTTCATCTCGCTCTCCGATCCA---GCACCAGAGGAAGAAC	269							
243	CCGTCAATTGGATTGGAGCGTTGTGAAGTACACCAAGTTGGACCACTGTGTTTGGCTT	302							
270	CATTGCAGATTTCACACGATACATGAGATTAATGATTTCAGCCGTTAAAGCGCTAACT	329							

[illegible]

ORIGIN

Query Match 11.8%; Score 109.2; DB 11; Length 810;
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Matches 308; Conservative 0; Mismatches 288; Indels 6; Gaps 2;

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Date: Jan 21, 2002 1:40 AM

About: Results were produced by the GenCore software, version 4.5.
Copyright (c) 1993-2000 CompuGen Ltd.

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ACCESSION A96985

VERSION A96985.1 GI:6780426

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

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CDS

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 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 1179)
 de Veylder, L., De Almeida Engler, J., Bursens, S., Manevski, A.,
 Lescure, B., Van Montagu, M., Engler, G. and Inze, D.
 A new D-type cyclin of Arabidopsis thaliana expressed during
 lateral root primordia formation
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1179)
 AUTHORS de Veylder, L.
 TITLE Direct Submission
 JOURNAL Submitted (16-DEC-1998) De Veylder L., Department of Genetics, VIB,
 Laboratorium voor Genetica, K.L. Ledeganckstraat 35, Gent B-9000,
 BELGIUM

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1 (sites)
and Tabata,S.
Kaneko,T., Kotani,H., Nakamura,Y., Sato,S., Asamizu,E., Miyajima,N.
AUTHORS
TITLE
STRUCTURAL ANALYSIS OF ARABIDOPSIS THALIANA CHROMOSOME 5. V.
SEQUENCE FEATURES OF THE REGIONS OF 1,381,565 BP COVERED BY TWENTY
ONE PHYSICALLY ASSIGNED P1 AND TAC CLONES
JOURNAL    DNA Res. 5 (2), 131-145 (1998)
MEDLINE    98344145
REFERENCE  2 (bases 1 to 88356)
Nakamura,Y.
TITLE      Direct Submission
AUTHORS    Submitted (02-MAR-1998) Yasukazu Nakamura, Kazusa DNA Research
JOURNAL    Institute, Department of Plant Gene Research, 1532-3, Yama,
Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
Tel:81-438-52-3935, Fax:81-438-52-3934)
COMMENT    Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see

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http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MNA5
 Genes with similarity to proteins in the databases are described in
 'product' or 'note' qualifiers. Genes that have no significant
 protein similarity are described as 'unknown protein'.
 The software programs used to predict genes include: Graal
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<http://compbio.cornell.gov/Graal-1.3/>),
 GENSCAN (Chris Burge, MIT, <http://CCR-081.mit.edu/GENSCAN.html>),
 NetGene2 (S.M. Hebscheid, et al., CBS, Technical University of
 Denmark, <http://www.cbs.dtu.dk/services/NetGene2/>) and
 SplicePredictor (Volker Brendel, Stanford University,
<http://greml.inl.zoal.iastate.edu/cgi-bin/sp.cgi>).
 Genes encoding tRNAs are predicted by tRNAscan-SE
 (Sean Eddy, Washington University School of Medicine, St. Louis,
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 This sequence may not be the entire insert of this clone. It may be
 shorter because we remove overlaps between neighboring submissions.
 The 5' clone is M0N23 and the 3' clone is K1904.

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JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 113053) EU Arabidopsis sequencing project.
AUTHORS	Direct Submission
TITLE	Submitted (28-APR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG. E-mail: lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7JY Norwich, UK, E-mail: michael.bevan@bsrc.ac.uk
COMMENT	Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/ Location/Qualifiers
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ACCESSION A85057
VERSION A85057.1 GI:6733798
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REFERENCE 1 (bases 1 to 1284)
AUTHORS Murray,J.A.
TITLE PLANTS WITH MODIFIED GROWTH
JOURNAL Patent: WO 9842851-A 1 01-OCT-1998;
MURRAY JAMES AUGUSTUS HENRY (GB); UNIV CAMBRIDGE TECH (GB)
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Quality: 722.50 Length: 341
Ratio: 2.961 Gaps: 10
Percent Similarity: 71.554 Percent Identity: 48.094
alignment_block:
US-09-530-209A-2 x NTA011892 ..
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1 MetAlaGluGluAsnLeu.....GluLeuSerLeuGlySer 13
||||| :|||:| :|||:| :|||:| :|||:| :|||:|
182 ATGGCAGCGATGATACATTATGATTTGTAGCCTCAACATCTTTATGTAC 231
13 rGluSerAsnVal.....AspAspGluGlyMetIleValAspG 26
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
232 AGAAACAAAAGCTCTTGTTCATGATGATGCTTTCATGACATATAAGTC 281
26 IuThrProIleGluIleSerIleProGluMetGlyPheSerGln..... 40
:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
282 AACAGACAACTTGAACTAAGAGTAAGACTTGAGCTTTTAAACAATGGCTATT 331
41 .....SerGluSerGluGluIleLeu 48
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
332 AGATTCAGACCATTGATTTGCCAAGTTTAAAGTGAAGAAATGCTTTGAG 381
48 tGluMetValGluLysGluLysGlnHisLeuProSerAspAspTyrIle 65
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
382 TTTTATGTGTCAGAAAGGAAATGGAGTTTGGCTTAAGATGATTATGTGC 431
65 yArGLeuArGserGlyAspLeuAspLeuAsnValGlyArgAspAla 81
:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
432 AGGATTTGAGAACTGGAGATTGGATTGGAGTGTG...AGAAAAGAGGCT 478
82 LeuAsnTrpIleTrpLysAlaCysGluValHisGlnPheGlyProLeu 98
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
479 CTTGATTTGGATTTTGAAGGCTCATATGACCATATGAGATTGGAGAGCTGAG 528
98 sPheCysLeuAlaMetAsnTyrLeuAspArgPheLeuSerValHisAsp 115
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
529 TTTTGTGTGTCATAATTTACTTGGATGATTTTCATCTCTGTATGAAT 578
115 euProSerClyLysGlyTrpIleLeuGlnLeuLeuAlaValAlaCysLeu 131
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
579 TGGCAAGAGATTAACCTTGACAGCTGCACATTTTACTGTGGCTGGCTGTCTA 628
132 SerLeuAlaAlaLysTrileGluGluTrpGluValProMetLeuLeuAsp 148
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
629 TCACCTTGACGCCAAATGAGAGAAATTAAATGTTCCTTGTGACTGTGATTT 678
148 uGlnValGlyAspProGlnPheValPheGluAlaLysSerValGlyArg 165
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
679 ACAGGTAAGGGAATCCCAATTTCTATTGAAGCAAAACATATCAAGAAG 728
165 etClnLeuLeuValLeuAsnLysLeuLysTrpArgLeuArgAlaIleThr 181
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BASE COUNT      554 a      283 c      308 g      552 t      2 others
ORIGIN

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      Ratio:      2.729      Gaps:      10
Percent Similarity:      71.176      Percent Identity:      44.118

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US-09-530-209A-2 x CRCYCD      ..

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403 CTTTATGGCGACAGATACCTACAGCATTTTGCATGACATTGATGATATA 452
      20 uGlyMet..IleValAspGluThrProIleGluIleSerIleProGln 36
         :      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
453 TTATTATGGGGTGTGTGACGATATGTCCTTCAGATTGTGAACCTGGAC 502
      36 et.....:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
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503 AACACATGGGAACTTGACAACTTGATTTTACATTATTTACTA 552
      37 .....GlyPheSerG1 40
553 ATATAATTCAGAACACAACTTTGAGGCTTTAAATTTCTGGGTTTGTG 602
      40 nserGluSerGluGluIleIleMetGluMetValGluGluGluGln 57
         :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
603 GGCA...AATCATGAGCTGTTGGCTTCCTGTTTGACAAATGAAGACAA 649
      57 IAsLeuProSerAspAspPylrIleLysArGluArGSerGlyAspLeuAsp 73
         :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
650 ATTTCCTGGGCTTGATTATTTGAAGAGATTCCGAAATGGGGATTTGGAT 699
      74 LeuAsnValGlyArgArgAspAlaLeuAsnTrpIleTrpLysAlaCysG1 90
         :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
700 TTGGGT...GCTAGAAATCTGGTTATGATGATGATCTCTAAGCTTCAATC 746
         :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
747 CCACATACATTTTGGGCCACTTTGGTTGATTATCTGTAACATACTTGG 796
      90 uValHisGlnPheGlyProLeuCysPheCysLeuAlaMetAsnTyrIleu 107
         :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
797 ATCCGCTTCCTTGGCTTATGATAATTACTT...GGCAAAAGCTTGACATG 843
      107 spArgPheLeuSerValHisAspLeuProSerGlyGlyG1TrpIleLeu 123
         :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
844 CAATTGCTTGGGGTGTGTTTATCTCTAGCTGCCAAGGAGGATGAACA 893
      140 rGluValProMetLeuIleAspLeuGlnValGlyAspProGlnPheValP 157
         :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
894 TGATGTTCCCTCATCTTGAATTTTACAAGTAGCAGTAAGTAAGTTGAT 943
      157 heGluAlaLysSerValGlnArgMetGluLeuValLeuAsnLysIleu 173

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944 TTGACGAAAAACATCAAGATGAAGTACTTTAGCTGTGACACTTTG 993
174 LysTTParGleuArGAlaIleThrProCysSerTylIleArgTyrPheLe 150
994 AACTGGAGATGCATCAATCAGTACGACATTTCTTCTTCTTCTTCTTCTT 1043
190 uArgLysMetSerLysCysAspGlnGluProSerAsnThrLeuIleSerA 207
1044 TTATAACCTGAGTGA...GATAAAATGCCATCAAAAAGCCTAATTTTTC 1090
207 rGserLeuGlnValIleAlaSerThrThrLysGlyIleAspPheLeuGlu 223
1091 AACCCATCCACATCATCTTACGACACATCAAGAAATGACTTGATGAGAA 1140
224 PheArgProSerGluAlaAlaAlaValAlaLeuSerValSerGlyGlu 240
1141 TTTCAGACCTTCAGAAATAGCAGACAGTGCATTTCTTCTTCTTCTTCTT 1190
240 uLeuGlnArgValHisPheAspAsnSerSerPheSerProLeuPheSerL 257
1191 AACCCAAATAGTAGAATCTACTGATAAGCATTCCTTTCTTCTTCTTCTT 1240
257 eubLeuGlnLysGluArgValLysIleGlyLumetile..... 270
1241 ATGTGGAAAAGAGAGATGATGAAATGCTTGAGATTAATGATGATTTG 1290
271 .....GluSerAspGly.....SerAspLeuCysSerGlu 280
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280 nThrProAsnGlyValLeuGluValSerAlaCysCysPheSerPheLysT 297
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297 hThiAspSerSerSerSer 303
1388 GTGATGATCATCATCAACACT 1407

seq_name: gp_pl:ATCD2
seq_documentation_block:
LOCUS ATCD2 1650 bp mRNA PLN 25-MAR-1998
DEFINITION A.thaliana mRNA for cyclin delta-2 (CYCD2).
ACCESSION X83370.1 GI:2995131
VERSION X83370.1 GI:2995131
KEYWORDS CYCD2; cyclin; cyclin D2; cyclin delta-2.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 1650)
Soul,R., Carmichael,J.P., Shah,Z.H. and Murray,J.A.
A family of cyclin D homologs from plants differentially controlled
by growth regulators and containing the conserved retinoblasoma
protein interaction motif
Plant Cell 7 (1), 85-103 (1995)
JOURNAL MEDLINE
REFERENCE 95210930
AUTHORS Murray,J.A.H.
TITLE Direct Submission
JOURNAL Submitted (08-DEC-1994) J.A.H. Murray, Inst. of Biotechn., Univ. of
Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
REMARK 3 (bases 1 to 1650)
AUTHORS Murray,J.A.H.
TITLE Direct Submission
JOURNAL Submitted (07-JUN-1996) J.A.H. Murray, Inst. of Biotechn., Univ. of
Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
REMARK 4 (bases 1 to 1650)
REFERENCE Murray,J.A.H.
AUTHORS

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TITLE Direct Submission
JOURNAL Submitted (19-MAR-1998) J.A.H. Murray, Inst. of Biotechn., Univ. of
Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
COMMENT On Mar 28, 1998 this sequence version replaced gi:1402895.
FEATURES
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Percent Similarity: 66.111 Percent Identity: 42.778
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US-09-530-209A-2 x ATCD2
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17 LAsPaSGluGlyMetIleValAspGluThrProLleGluIle..... 31
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31 ..... 31
271 GCGGCGGATTTACGACAGATGATTACATCAACCAACTTTTGTCTAA 320
32 .....SerIleProGlnMetLysPheSerGlu 40
321 GACGACAACTTTGGCGGCAACGATCAATCCATGATGAGTCTTCTTCT 370
40 nSerGlu...SerGluGluIleIleMetGluMetValGluLysGluLysG 56
|||||
371 ATGCTCTTGAGTGAAGACAGCAATCAAGAGATGTTGTTAGAGAGATTG 420
56 LhThiLeuProSerAspAspTyrIleLysArgLeuArgSerGlyAspLeu 72
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421 AGTTTCCCTCGAACACTGATTAAGAGATTGCTTCTGCGATTTG 470

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863 GAAGGACCATATAAAGATGGAGCTTCGTGTGCTAAGCAACCTTAAAGTG 912

176 ArgLeuAlaArgAlaIleThrProCysSerTrpIleArgTyRPhLeuArgly 192
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913 AGCATCCATCGACTTTACTGCTTCATTGTTGAATTAATTCTTCATFA 962

192 smetserLysCysAspGlnGluProSerasnThrLeuIleSerArgSertL 209
||||| ||||| |||||
963 ATTGAGTGTAT... CATGTGCACCCCTTCCTTGTCTTGCACCGCTCGCTCTT 1009

209 euGIvalIlealaserThrThrLysGlyIleasppHeuGluPheArg 225
.....: |||||.....: |||||.....: |||||
1010 CGGACCTTCTCTTGAGCACCGCTAAAGGTGCTGAATTCGCGATTTCAGA 1059

226 ProSerGluAlaAlaAlaValAlaLeuSerValSerGlyLeuGl 242
||||| |||||.....: |||||:
1060 CCTTCGAGATTGCTGCCAGTGTGCACCTTGCCTGCTATCGCAGAAATGCAG 1109

242 nArgValHisPheaspasnSerSerPheSerProlenPheSerLeuLeuc 259
: ..:::.....: ||| :..: |||:
1110 GAGTTCGTGAATTGAGAGAGCTGCTGATGAGCTGCCAAATAT..... TTGg 1153

259 IuLysGluArgValLysLysIleGlyIleMetIleGlu..... 271
: |||||.....: |||||.....: |||||.....:

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272SerAspGlySerAspLeuCysser..... 279
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280 .GlnThrProAsnGlyValLeuGluValSerAlaCys..... 291
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292 CysPheSerPheLysThr 297
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seq_name: gb_pl:AC006592

seq_documentation_block:

LOCUS AC006592 12051 bp DNA PLN 05-APR-2000

DEFINITION Arabidopsis thaliana chromosome II section 127 of 255 of the complete sequence. Sequence from clones F14M13.

ACCESSION AC006592 AE002093

VERSION AC006592.5 GI:6598614

KEYWORDS HTG.

SOURCE thale cress.
ORGANISM Arabidopsis thaliana

REFERENCE Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 102051)
Lin,X., Kaul,S., Rounsley,S.D., Shea,T.P., Bentto,M.-I., Town,C.D., Fujii,C.Y., Mason,T.M., Bowman,C.L., Barnstead,M.E., Feldblum,T.V., Buell,C.R., Ketchum,K.A., Lee,J.J., Renning,C.M., Koo,H., Moffitt,K.S., Cronin,L.A., Shen,M., Vankken,S.E., Umayam,L., Tallon,L.J., Gill,J.E., Adams,M.D., Carreira,A.J., Creasy,T.H., Goodman,H.M., Somerville,C.R., Coppenhafer,G.P., Preuss,D., Nierman,W.C., White,O., Eisen,J.A., Salzberg,S.L., Fraser,C.M. and Venter,J.C.

TITLE Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana

JOURNAL Nature 402 (6763), 761-768 (1999)

MEDLINE 20083487

PUBMED 10617197

REFERENCE 2 (bases 1 to 102051)

AUTHORS Lin,X.

TITLE Direct Submission

JOURNAL
COMMENT

Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
On Dec 17, 1999 this sequence version replaced g1:4544435.
The sequence and annotation of chromosome 2 were gained from tho-
n of the individual clones on this chromosome after removing
overlaps. For detailed information, please see the TIGR web site
(<http://www.tigr.org/cdb/at/na.html>).

Genes were identified by a combination of three methods: Gene prediction programs including GNAI, (<ftp://arthur.epm.ornl.gov/pub/xyrali>), GeneFinder (Phil Green, University of Washington), GENSCAN (Chris Burge, <http://genome.stanford.edu/GENSCANW.html>), and NetPlantGene (<http://www.cbs.dtu.dk/services/NetGene2/>), searches of the complete sequence against a peptide database and plant EST databases at TrGR, and manual curation based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>). Simple repeats were identified by RepeatMasker (Arian Smit, <http://ftp.genome.washington.edu/RM/RepeatMasker.html>). Genes are numbered from the top to bottom of the chromosome.

We thank the GSHL/MasNV/ABI consortium for sequencing BMC clones F6P23, F5J6, T17A5, and T13J16, the ESSA group for sequencing clone F13Dd, and Scott Jackson, Jining Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Jiang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and database support.

This work was supported by the National Science Foundation, Department of Energy and the US Department of Agriculture.

Address all correspondence to: at@tigr.org.

FEATURES
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1. .102051

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2007

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2018

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      CNGGEISPTGCTGSGDGRVAKRISLAKPAGVDSGSRVKGEGNAGRGSPDL
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               /db_xref="GI:4544452"
               /translation="MADEVDYFQVINGDSAVGSKLARFTRDEFMSDKATIRC
               RFQYSNAPYKGAAMLYDMTIRSFPHIQMPELRYHADKNIVILLIGNKTDL
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               CSSQVSLIRPPCVAAQ"

alignment_scores:
  Quality: 501.50      Length: 569
  Ratio: 2.047         Gaps: 19
  Percent Similarity: 43.058   Percent Identity: 28.120

alignment_block:
US-09-530-209a-2 x AC006592/rev ..

Align seg 1/1 to reverse of: AC006592 from: 1 to: 102051

1 MetAlaGlunGluAsnLeuGluSerLeuGlySThGluSerAsnVa 17
  |||||
68537 ATGCGTGAG.....AATCTTGCTGTGCTGAACACGAGC... 68505

17 IAspAspGluGlyMetIleValAspGluThrProLeuGlu..... 31
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68504 .....GAGTCATGATCATTTGACACGACGATGATCATCACTAG 68462

31 ..... 31

68461 GCGCGGATTTAGCAACGATTTGATTACATCACTTTTGTCTAA 68412

32 ..... SerIleProGluMetGlyPheSerGI 40
  |||||
68411 GACGACAACTTTGGCGGCAACGATCATTCGATGTGGCTCTTCTTC 68362

40 nSerGlu...SerGluIuIleIleMetGluMetValGluIuGluLysG 56
  |||||
68361 ATGCTCTTGAAGTAAACAGATCAAGATGATGTTGTCGACAGATTC 68312

56 InHISLeuProSerAspAspTyrIleLysArgLeuAspSerGlyAspLeu 72
  |||||
68311 AGTTTGGCCCGGAACTGATATGTTAAGAGATTGCTTGTGGGATTG 68262

73 AspLeuAsnValGlyArgArgAspAlaLeuAsnTrpIleTrpLysAlaCy 89
  |||||
68261 GATTTGTCTGTT...CGAACCAGCTCTTGATTTGATCTAAAGCTATG 68215

89 sGluVal..... 91
  |||||
68214 TGATTTCTTCTTTGATGCTTTGATGCTGTGTGTTTAAGACAAACC 68165

91 ..... 91
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68164 TCAAAATCGTTTGCTCTCTTTTGTGCTTTGTGATTTAGTGTG 68115
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91 ..... 91
68114 TTCTTTCAGTTGATGACCTCATTCATTCCTGATGATATTATTATAG 68065
91 ..... 91
68064 ATTAAATTGAATCTTCCTATAGATTGAGTATGATCTGTGAGTAAT 68015
92 ..... His 92
68014 GAGTCTTTTGTCTTAATGCCAATGTTCTACAGTTTGTCTCATTTAC 67965
93 GlnPheGlyProLeuGlyPheGlyLeuAlaMetAsnTyrLeuAspArg 109
67964 CATTTCGACATCTGTGCATATGCTATCCATGACTTGTGATCGGTT 67915
109 eLeuSerValHisAspLeuPro..... 116
67914 CTTAAACATCCTATGAATGGCCGGTAAGTTGCATCGTCTTGGGATTCGT 67865
116 ..... 116
67864 TTCATCGTATTCGACAAATACGATGACCGGTTTGTGTTTCGATTGC 67815
117 ...SerGlyLysGly_TripLeuGlnLeuAlaValAlaCysLeu 132
67814 GTGAAAGACAAAGAGATTGGCTGCTCAGTTACTGCTGCTGCTTAT 67765
132 eLeuAlaAlaLysIleGlnIuThrGluValProMetLeuLeuAspLeu 148
67764 CATTAGCATCCAAATGAGAAACATGATGCTCATTTGATTGATTTA 67715
148 ..... 148
67714 CAGGTGCACTTACTTATGCTTATAGCTTCTTCTTACAGAGA 67665
148 ..... 148
67664 GTGCAAAATGAGGTTTACTGCACTAATCTGAATGTTGTTCCATG 67615
149 ..GlnValGlyAspProGlnPheValPheGlnAlaLysSerValGlnArg 164
67614 AGCAGGTGGAAGATCCCAAGTTGTTTATGAGGCAAAACAAATAAAG 67565
165 MetGlnLeuLeuValLeuAsnLysLeuLysTyrArgLeuArgAlaIle 181
67564 ATGGAGCTTTTGGTGTGCACCACTTGAATGGAGATTGCAAGCTTAA 67515
181 rProCysSerTyrIleArgTyrPheLeuArgLysMetSerLysCysAsp 198
67514 TCCATTCTCTCTTCAATTATTTGTTGACAGACATCAGT.....G 67474
198 InGluProSerAsnThrLeuIleSerArgSerLeuGlnValIleAlaSer 214
67473 GTACAGGTGCGAGAAATTTGATATAGATCGTCAACATTCATTAAAC 67424
215 ThrThrLysGly..... 218
67423 ACCACCAAGGTGCGTATTATGATCAGACAGCACTATACACATTT 67374
218 ..... 218
67373 CTTTCTTATTTCGACTAACTGGCTTTGTTTATAGACAGGCTGATA 67324
219 ..... IleAspPheLeuGlnPheArg 225
67323 CGTTTCTGTTTATAAATGATGACAGCAATTTGATTTAGACTTACG 67274
226 ProSerGlu.....AlaAlaAlaValAlaLeuSerValSerGlyG 240
67273 CCTTCTGATAGCTGACGCTGCGAGTGTCTTTCATTTCAGGAGA 67224
240 uLeuGln..... 242

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67223 AACAGAAATGATGATGAGAAAGACGCTGTCTAGTCTATATATGTA 67174
243 .....ArgValHisPheAspAsnSerSerPheSerProLeu... 254
67173 AACAGTAATTAACATTCGGTATGATGACGAAAGACCTTAACCTTACTG 67124
255 .....PheSerLeu.....LeuGlnLysGluArg 262
67123 TTTCAGACACACATTTTCATCTGATCATTTCTTCTCTTACAGAGAGAG 67074
262 gValLysLysIleGlyGlnMetIleGlnSer..... 272
67073 GGTGAAGAGATGTTTGAATCTGATGACAGACTTCACATGCGGAGAGATG 67024
273 ..AspGlySerAspLeuGlySerGln..... 280
67023 TGCAGGAGACTTATTCGACAGACGCGCAGTTGCGTAAGAGCT 66974
281 .....ThrProAsnGlyValLeuGlnValSerValLacysCysPhe 294
66973 GTACCTCAAGTCCAGTTGAGAGTTGGAA.....GCAACATGTTTACG 66930
294 rPheLys.....ThrHisAspSerSers 302
66929 CTATAGAGAGTGAAGAGAGACAGTTCATGATGATCAAAATTCCTCACGA 66880
302 eSer 303
66879 GTACT 66875
seq_name: gb.pl:ATCD1
seq_documentation_block:
LOCUS ATCD1 1951 bp mRNA PLN 25-MAR-1998
DEFINITION A.thaliana mRNA for cyclin delta-1.
ACCESSION X83369
VERSION X83369.1 GI:2995129
KEYWORDS cyclin; cyclin delta-1.
SOURCE
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1951)
Sonl,R., Carmichael,J.P., Shah,Z.H. and Murray,J.A.
A family of cyclin D homologs from plants differentially controlled
by growth regulators and containing the conserved retinoblastoma
protein interaction motif
Plant Cell 7 (1), 85-103 (1995)
JOURNAL
MEDLINE 95210930
REFERENCE
2 (bases 1 to 1951)
Murray,J.A.H.
Direct Submission
Submitted (08-DEC-1994) J.A.H. Murray, Inst. of Biotechn., Univ. of
Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
REMARK
3 (bases 1 to 1951)
revised by [3]
Murray,J.A.H.
Direct Submission
Submitted (19-MAR-1998) J.A.H. Murray, Inst. of Biotechn., Univ. of
Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
On Mar 28, 1998 this sequence version replaced g1:603504.
COMMENT
FEATURES
location/Qualifiers
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/organism="Arabidopsis thaliana"
/variety="ecotype landsberg erecta"
/db_xref="taxon:3702"
/dev_stage="seedlings, stage 2 leaves"
/issue_type="whole seedlings"
/clone_lib="pFlu1"
104..1111
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CDS

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alignment_block:
US-09-530-209A-2 x A85060 .
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Align seg 1/1 to: A85060 from: 1 to: 1788

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198 TTAAGTCTGCGCGAG.....GACTCGGCATATATATACCGGCGCA 225
26 uThrProIleGluIleSerIleProGlnMetGlyPheSerGlnSer...G 42
236 CGACGGCGCGGAGTGTCTCC.....TATGATTCGAATATATCCGGCG 276
42 LuSerGluGluIleIleMetGluMetValGluGluGluGlnIleSleu 58
277 ACTTGTATGATTCGATCGCGAGTTTATACAGACGAGAGAAAGTTCGTT 326
59 ProSerAspAspTyrIleLeuYsArgLeuArgSerGlyAspLeuAspLeu 75
327 CCAGGATTCATTCATTCGAGCGATTCATTCATTCGATTCGATTCGTTTC 376
75 nValGlyArgArgAspAlaLeuAsnTrpIleTrpLysAlaCysGluValH 92
377 T...GCTAGAGAAAGATCGGTGCTGCGATCTTAAGGTCAACGGTTT 423
92 IscGlnPheGlyProLeuCysPheCysLeuAlaMetAsnTrpLeuAspArg 108
424 ACGAATTCAGCGCGTTCACGCGTACCTCCGTTACTATTCGATTCGATCGT 473
109 PheLeuSerValHisAspLeuProSerGlyLysGlyTrpIleLeuGlnLe 125
474 TTCATCTATTGCGGTGCTTCGCGTGCAGAAATGCGGCGCCCTTCGACACT 523
125 uLeuAlaValAlaCysLeuSerLeuAlaAlaLysIleGluIleThrGluV 142
524 CTATCTGTCGATGCTGCTGCTTACGTCCTAAATGAGAGAAACCTTTA 573
142 alProMetLeuIleAspLeuGlnValGlyAspProGlnPheValPheGlu 158
574 TTCCTTCTATTCTTGATCTCAGGTTGCAAGTGCAAAATATATTTTCGAG 623
159 AluLySerValGlnArgMetGluLeuLeuValLeuAsnLysLeuLysTr 175
624 CCGAAACCAATCCGAGAAATGAGATTCTTGTGCTTATAGTTTGGATTCG 673
175 PaGluArgAlaIleThrProCysSerTrpIleArgTrpPheLeuArgL 192
674 GAACTAAGATCCGTTACACGTTTACCTTTATCGGCTCTTTTCGCACA 723
192 YsMetSerLysCysAspGlnIleProSerAsnThr.....Leu 204
724 AATATC.....GATCATCTGGAATGTATACGGCTTCTCT 758
205 IleSerArgSerLeuGlnValIleAlaSerThrTrpLysGlyIleAspH 221
759 ATCTCAAGGCGCAACAAATATATCTCTCAAAATATTCAGACAGCTAGTTT 808
221 eLeuGluPheArgProSerGluAlaAlaAlaValAlaLeuSerValS 238
809 ACTTGAATATGGCCATCATGATGTTGCTGCTGCAACATATCTTGTTCAG 858
238 eGlyGluLeuGlnArgValHisPheAspAsnSerSerPheSerProLeu 254
859 CAAGTATCTTTTAAATCTCACTTATCAATGCTGATCTGCTGATCA 908
255 Phe...SerLeuLeuGlnLysGluArgValLysLysIleGlyLysMetI 270
909 TGGTGTGATGCGCTTACCAAGAGAGATCAAAATATGTACAGACTTGT 958
270 eGluSerAspGlySerAspLeuYsSerGlnTrpProAsnGlyValLeuG 287
959 ACATATCTCCAAA.....G 971
287 LuValSerAlaCysCysPheSerPheLysThrHisAspSerSerSer 303
972 ATATTCGCGGTACATGTTTCAGT.....CATGACGGCTCGAGTACAG 1012

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304 Tyr 304
111
1013 TAC 1015

seq_name: gb_pl:AMA250396

seq_documentation block:

LOCUS AMA250396 1162 bp mRNA PLN 15-NOV-1999

DEFINITION Antlirrhinum majus mRNA for cyclin D1 (cyclin gene).

ACCESSION AJ250396

VERSION AJ250396.1 GI:6448479

KEYWORDS cyclin gene; cyclin D1.

SOURCE snapdragon.

ORGANISM Antlirrhinum majus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Lamiales; Veronicaceae; Antlirrhinum.

1 (bases 1 to 1162)

REFERENCE 2 (bases 1 to 1162)

AUTHORS Doonan,J.H.

TITLE Direct Submission

JOURNAL Submitted (18-OCT-1999) Doonan J.H., Cell Biology, John Innes

Centre, Colney Lane, Norwich, NR4 7UH, UNITED KINGDOM

location/Qualifiers

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/dev_stage="flower spike"

139..1131

/gene="cyclin D1"

139..1131

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/codon_start=1

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/protein_id="CAB61221.1"

/db_xref="GI:6448480"

/translation="MSLSGDSGFSLLGDSNITFSGGDDLPRTSDVESIPDVD

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DRFLNAHLPLKNGMPQMLSVACLSLAKMESLVPSLDQVAGANTEPRNIOR

MELIVRLVDNRLRSISPCYLSFALKIDPTGYTGTFSRAKEIILSTVOETSLIE

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BASE COUNT 333 a 268 c 246 g 315 t

ORIGIN

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Quality: 399.50 Length: 304

Ratio: 2.136 Gaps: 10

Percent Similarity: 61.513 Percent Identity: 34.868

alignment_block:

US-09-530-209A-2 x AMA250396 ..

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124 GACGAACGACTCGGCATGTCACGTGCTGCTCGCATTCGTTCTCCATTC 173

19AspGluGlyMetIleVal.....AspGluTr 27

174 TCCTCTGCGGCGAGGATTCAAATATATATATCTCCGCGCGAGATGACC 223

27 hrPro.....IleGluIleSerIleProGlnMetGlyPhe 38

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seq_name:	gb_pl:ATCD3	
seq_documentation_block:	1632 bp	mRNA
LOCUS	ATCD3	PLN
DEFINITION	A.thaliana mRNA for cyclin delta-3.	
ACCESSION	X83371	
VERSION	X83371.1	GI:2995133

KEYWORDS cyclin; cyclin delta-3.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1632)
Sonl,R., Carmichael,J.P., Shah,Z.H. and Murray,J.A.
A family of cyclin D homologs from plants differentially controlled
by growth regulators and containing the conserved retinoblastoma
protein interaction motif
Journal Plant Cell 7 (1), 85-103 (1995)
MEDLINE 95210930
REFERENCE 2 (bases 1 to 1632)
AUTHORS Murray,J.A.H.
TITLE Direct Submission
Submitted (08-DEC-1994) J.A.H. Murray, Inst. of Biotechn., Univ. of
Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
REMARK revised by [3]
REFERENCE 3 (bases 1 to 1632)
Murray,J.A.H.
TITLE Direct Submission
Submitted (19-MAR-1998) J.A.H. Murray, Inst. of Biotechn., Univ. of
Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
COMMENT On Mar 28, 1998 this sequence version replaced gi:503508.
FEATURES
location/Qualifiers
1..1632

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/db_xref="GI:2995134"
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ETKVEFEKTIQREMLLITLLEMKMLITLIPSFVDHILIRGLKNNAMHDFLNCH
LLSYISRPVGYPLSPVAAMTMRIIEVDPEPLSYOTNLGLVNLNTEKRYTCY
DLIILDPDRICLIDOTQSSKRRKSHSSSNLSPCYIDAMPNDESSNDSWGAAS
CNPPTSSSPQDPPLKMKGAENEKKIILHLPAAIATP"
329..343
/note="LxCxE motif"
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347..472
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misc_feature
521..838
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misc_feature
1169..1393
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BASE COUNT 478 a 369 c 317 g 468 t
ORIGIN

alignment_scores:
Quality: 398.00 Length: 322
Ratio: 2.041 Gaps: 11
Percent Similarity: 60.559 Percent Identity: 32.919

alignment_block:
US-09-530-209A-2 x ATCD3 ..
Align seg 1/1 to: ATCD3 from: 1 to: 1632

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326 GCCTCTACTGCAGAAAGACAAATGGGACCATTCAAGACAAGAAGTTGA 378
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[illegible]

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1171 CGATTCATCATCATCG 1186
seq_name: gb_p1:AMA250397
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seq_documentation_block:
LOCUS       AMA250397               1140 bp      mRNA      15-NOV-1998
DEFINITION  Antirrhinum majus partial mRNA for cyclin D3a (cycD3a gene).
ACCESSION   AJ250397
VERSION     AJ250397.1  GI:6448481
KEYWORDS
SOURCE      snapdragon.

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ORGANISM	REFERENCE	TITLE
<i>Antirrhinum majus</i>	Gauthier, V., Lunniss, P., Robert, P., Towers, M., Riou-Khamlich, C., Murry, J., Coen, E. and Doonan, J.H.	The expression of D-cyclin genes define distinct developmental
<i>Eukaryota</i> : Viridiplantae; Streptophyta; Embryophyta; Tracheophyta.		
<i>Spermatophyta</i> ; Magnoliophyta; eudicotyledons; core eudicots.		
<i>Asteridae</i> ; easterids I; Lamiales; Veroniceae; <i>Antirrhinum</i> .		
I (bases 1 to 1140)		

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1140)
AUTHORS Doonan, J.H..
TITLE Direct Submission
JOURNAL Submitted (18-OCT-1999) Doonan J.H., Cell Biology, John Innes
Centre, Colney Lane, Norwich, NR4 7UH, UNITED KINGDOM

FEATURES	Location/Qualifiers
source	1. .1140

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/gene="cycd3a"
110..>1139
CDS

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FSATPAVIAVAVIADRFICTROFODKPMWVOLAVALCTSLAAKVEENOVPLLDIOWE
ESKIVFESKTIQREHLLVSTLTKMKNPVPTISLETIARLAKLSHCKEFLURCEC
LLSLITDCRFMCHLPSALATATMLVVISSEPGVAYQDLINLIGINDKRECC
KLIOEATVSVHFOSGNRKREKESLPYSPRGVVDISFCDSDNPSLDSTASVSSPEHLISK
KIKYQNDNH"

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BASE COUNT	332 a	223 c	237 g	348 t
ORIGIN				

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Ratio:	1.860
Percent Similarity:	63.444
	Length: 3311
	Gaps: 10
Percent Identity:	32.024

alignment_block:
US-09-530-209A-2 x AMA250397

Align seg 1/1 to: AMA250397 from: 1 to: 1140

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146 GCCTGTACTGATGGAGAACAACAAACTGGCAATGGTGAATCATCAA 195
25 pglutHrProIleGluIleSerIleproGlnmetcIlyPheSerInsrg 42
TGACTGTTTCATTGAGAACCAAGACC.....TTTTTCATTATTAT 236

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42 lusergluglujele...melglumetvalglugylsglulsgin 56
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237 TGAACACTGATTTCATTATGTCGTGTAGATCATGATGATGATGATGATAAAGAA 286

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101  CTCAGATGGGTTTTTCTCATATCGAGAGTACGAGCATATATCATGGAGATG 150
51  ValGluLysGluLysGlnHisLeuProSerAspSerPylIleLysArgLe 67
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151  GTGAGAGAGAGAGAGAGCATTTGGCCAGATGATATACCTACAGAGACT 200
67  uArgSerGlyAspLeuAspLeuAsnValGlyArgAspAlaLeuAsnT 84
    |||||||
201  TAGAAGTGGAGATTGGATTGGAATGTGSAAGAAGAGATGCCCTCAATT 250
84  rPileTrpLysAlaCysGluValHisGlnPheGlyProLeuCysPheCys 100
    |||||||
251  GGATTTGGAAGGCTTGTGAAGCTACACCACCTTGGACCATTGTGTTTTGC 300
101  LeuAlaMetAsnTrpLeuAspArgPheLeuSerValHisAspLeuProSe 117
    |||||||
301  TTACCAATGAACACTACTGTGATCGATTTCTTATCGGTTATGATTTCCCTAG 350
117  rGlyLysGlyTrpIleLeuGlnLeuAlaValAlaCysLeuSerLeuA 134
    |||||||
351  TCGCAAGGTTGGATATTGCGATTGGCTGTGGCTGTTTATCATTTGG 400
134  AlaAlaLysIleGluGluThrGluValProMetLeuIleAspLeuGluVal 150
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401  CAGCCAAATTTGAAGAAACCTGAATCTCAATGTGATGATCTTCAGGTT 450
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167  uLeuValLeuAsnLysLeuLysTrpArgLeuArgAlaIleThrProCys 184
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501  TTTGGTGTGAACAATTTGAATGAGATGAGAGCAATTAATCTCCATGCT 550
184  eTrpTrpIleArgTrpPheLeuArgLysMetSerLysCysAspGlnGluPro 200
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551  CATACATTAAGATATTTCTCTGAGAAAGATGAGTAAATGTGATCAGAACCA 600
201  SerAsnThrLeuIleSerArgSerLeuGlnValIleAlaSerThrThyL 217
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601  TCCACACACATTTGATATCTAGATCATTAAGATAGCAGACCAACCA 650
217  sGlyIleAspPheLeuGluPheArgProSerGluAlaIleAlaIleValA 234
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651  AGGTATTTGACTTTTGGAGTTTGAACCTTCTGAACCTGCTGCTGTGG 700
234  LeuSerValSerGlyLeuLeuGlnArgValHisPheAspAsnSerSer 250
    |||||||
701  CACTTTCTCTTTCTGAGAAATTCAGAGAGTACACTTGCACAACCTCTCC 750
251  PheSerProLeuPheSerLeuLeuGlnLysGluArgValLysLysIleG 267
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751  TTCTCTCTCTTTTCTCACTACTTCAAAAGGAGAGTGAAGAAGATAGG 800
267  yGluMetIleGluSerAspGlySerAspLeuLysSerGlnTrpProAsnG 284
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801  GGAATAGATGAGAGTGAATGCTGCTCAGACTTATCTCACAACCAACCAATG 850
284  IValLeuGlnValSerAlaCysCysPheSerPheLysThrHisAspSer 300
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851  GGGTTTTAGAGATATCGGCTTGTGTTTCAGCTTTAAGACCCATGATCT 900
301  SerSerSerLysTrpThrHisLeuSer 308
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ID AAC48940 standard; DNA: 1287 BP.
XX
AC AAC48940;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 59332.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
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201 serasnthleuileserargserleuenglinalleaserththly 217
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844 TCCAAACATGTGATATCTAGATCATTAACAGTATAGCCAGACCAACCA 893
217 sgllyleasphelueglupheargproserglualalalalalalalal 234
|||||
894 AGGTATTGACTTTTGGAGTTTACACTTCTGAAAGTCTGCTGCTGAG 943
234 laleuservalserglulysglulysgluvalhisphaspsnser 250
|||||
944 CACTTCTGTTCTGAGAAATTCAGAGAGTACACTTTGACAACTCTTCC 993
251 pheaserproleupheserleuenglulysgluargvallysllecl 267
|||||
994 TTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1043
267 yglumetleuuseraspglyserasplespousserglinthproasng 284
|||||
1044 GGAATGTAGAGAGAGTATGAGTCTGAGCTTATTTTCCAAACCAACCA 1093
284 lyvalleuenglulysvalseralacyscyspheserphelysthrhisaspser 300
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1094 GGGTTTGAAGTATCGGCTTGTGTTTCAAGCTTAAAGACCATGATCT 1143
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seq_name: /SIDS2/gcgdata/geneseq/genesegp/NA1998.DAT.AAV33884
seq_documentation_block:
ID AAV33884 standard; cDNA to mRNA; 1284 BP.
XX
AC AAV33884;

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XX 25-JAN-1999 (first entry)
XX N. tabacum CYCD2.1 gene.
DE D-type cyclin; growth; plant; cell-division control; phosphorylation;
KW CDC; Rd; retinoblastoma; germination; flowering; seed; fruit;
KW root development; ds.
XX Nicotiana tabacum.
OS
PN MO9842851-A1.
PD 01-OCT-1998.
XX 24-MAR-1998; 98MO-EP01701.
PF 26-MAR-1997; 97EP-0302096.
PR (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX Murray JAH;
XX WPI; 1998-532012/45.
XX DR Regulating growth and structure of plants by modulating protein that
XX PT controls cell division - specifically a D-type cyclin, and related
XX PT chimeric genes and transformed cells and plants, used to alter
XX PT growth rate, flowering, seed production etc.
XX PS Claim 14; p52-53; 75pp; English.
XX
CC This sequence represents the CYCD2.1 cDNA from Nicotiana tabacum which
CC encodes a D-type cyclin. The sequence can be used to alter the growth
CC characteristics or architecture of plants by altering the (functional)
CC level in the plant cells of a cell-division controlling protein that can
CC bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin.
CC Modulation of the cyclin gene is used to increase or decrease the growth
CC rate, provide faster germination, reduce time to flowering, increase the
CC number of flowers, seeds or fruits per plant, increase root development,
CC reduce height and to delay flowering in a range of plants, e.g. legumes,
CC grasses, maize, oilseed rape, wheat, tomato, rice, barley, sunflower,
CC carnation, chrysanthemum, rose, tulip, etc.
XX SQ Sequence 1284 BP; 415 A; 179 C; 261 G; 429 T; 0 other;
XX
alignment_scores:
Ratio: 722.50 Length: 341
Ratio: 2.961 Gaps: 10
Percent Similarity: 71.554 Percent Identity: 48.094
alignment_block:
US-09-530-209A-2 x AAV33884 ..
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182 ATGCGAGCTGATTAACATTTATGATTTGTAGCCCTCAATCTTTATGTAC 231
13 rgluserasnval.....AspaspGlnGlymetGlyphesergln..... 40
|||||
232 AGAACAACAAAGAGCTTTGTTGATGATGATGATGATGATGATGATGATG 281
26 luthrprolleuGlulleserleuproglnmetGlyphesergln..... 40
::: |||||
282 AACAGACATTTGAACATAAGATAAGACTTGACCTTTAAACAATGATAT 331
41 .....sergluserglulullelleme 48
||| |||||
332 AGATGAGACCATGATGATTTGCAAGTTTAAGTGAAGAAATGCTTGAG 381

```

```

48 tglumetvalglulysglulysglulhisleuprosersaspptyrillel 65
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382 TTTTATGGTGCAGGAAATGAGTTTTCCTTAAGATGATTAATGTCG 431
   :|||.....||| :||| |||||.....|||
65 ysatrgleuargserglyasppluaspluasvalglararaspala 81
   :|||.....||| :||| |||||.....|||
432 AGAGATTGAGAACTGAGATTGATTGATTGAGTGTG...AGAAAAGAGGCT 478
   :|||.....||| :||| |||||.....|||
82 leuasttrpilletrpilysalacysglulvalhisglinphelglyproleucy 98
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479 CTGTGATTGGATTTTGAAGCTCATATGCATATGATTTGGACAGCTGAG 528
   |||.....||| ||||| :||| |||||.....|||
98 spheCysleualamelasntylrleuasparpheluservalhisaspl 115
   |||||.....||| ||||| |||||.....|||
529 TTTTGTTCGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 578
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115 euproseryglyslytrpilleugluleuvalavalaalacysleu 131
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579 TGCCAGAGAACTTAAGCTGACAGTCAATTTGACCTGTGCTGCTGCTA 628
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132 Serleualalalalysilleglulthrleuvalprometleuileasple 148
   |||||.....||| ||||| :||| |||||.....|||
629 TCACCTTGACGCAAAATGGAAGAAATTAATGTCCTTGTGATTTT 678
   |||||.....||| ||||| :||| |||||.....|||
148 ugluvalglaspaproglinphelvalphelualalysservalglarqm 165
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679 ACAGGTAGGGGATCCCAATTTTATTTGAGGCAAAACTATATCAANGAA 728
   |||||.....||| ||||| |||||.....|||
165 etgluleuvalleuasnllysleulstrpargluaralalalthr 181
   |||||.....||| ||||| |||||.....|||
729 TGGAACCTTTGGTATTAAGCACATTTGAAGTGAAGTCAAGCTTTATACA 778
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182 ProCysSerTyrlleargtyrpheluearglysmeserlyscysaspl 198
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779 CCTTACACATCATAGTATTTATTAAGAAAGATGATGATGAT...GATCA 825
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198 nguluprosersasnthrleuileaserargserleuvalalalaser 215
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826 AATCCATCTCGGCGGCTGATTTCTGATCAATGCAACATGATTTAAGCA 875
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215 hthrlysglyleaspheluegluphearproserglualalalala 231
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876 TAATAGAACTATTGATTTCTTGAATTCAGCTCTTGAATTCGACGCA 925
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232 AlaValAlaLeuSerValSerGlyLuleuGlnArgValHisPheaspas 248
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926 TCAGTGGCATGTCTGTTTCAGGGAAATCAAGCAAAAGACATTTGATTA 975
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248 nserSerPheSerProleupheSerleu...leuGlnLysGlnArgVal 264
   :||| :||| ||| :|||.....||| |||||.....|||
976 GGCA.....ATGCTTGTCTTCTTACATCACTTAAGCAAGGTAAGTGC 1019
   :|||.....||| ||||| |||||.....|||
264 ysllysilleglylumelelelu..... 271
   :||| :||| ||| :|||.....|||
1020 AGAAGTGTGTTGAACGATTCAGAGATTGACAACTGCTACTATTACTACT 1069
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272 SerAspGlySerAspLeuCySerGlnThrProAsnGlyValLeuGluVal 288
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1070 GCGTGTGCTGCTCCTCATTAATTAAGTCAATTCAGTGTGTTGAA... 1117
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288 lserAlaIacCysPheSerPheLysThrHisAsp..... 299
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1118 .GCAGCAGCATGTGCTGAGCTACAAAGTGTGATGAGAGAAAGTGGAT 1166
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300 .....SerSerSerSerTyrlThr 305
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seq_name: /STD2/gc9data/geneseq/geneseqn/NA1998.DAT:AAV33889
seq_documentation_block:
ID AAV33889 standard; cDNA to mRNA; 1846 BP.
XX

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AC AAV33889;
XX
DT 25-JAN-1999 (first entry)
XX
DE Maize CYCD2 gene.
XX
KW D-type cyclin; growth; plant; cell-division control; phosphorylation;
KW CDC; Rb; retinoblastoma; germination; flowering; seed; fruit;
KW root development; ds.
XX
OS Zea mays.
XX
PN W09842851-A1.
XX
PD 01-OCT-1998.
XX
PF 24-MAR-1998; 98WO-EP01701.
XX
PR 26-MAR-1997; 97EP-0302096.
XX
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
PI Murray JAH;
XX
DR WPI: 1998-532012/45.
XX
PT Regulating growth and structure of plants by 'modulating protein that
PT controls cell division - specifically a D-type cyclin, and related
PT chimeric genes and transformed cells and plants,' used to alter
PT growth rate, flowering, seed production etc.
XX
PS Claim 14; p64-65; 75pp; English.
XX
CC This sequence represents the CYCD1;1 cDNA from Zea mays which encodes
CC a D-type cyclin. The sequence can be used to alter the growth
CC characteristics or architecture of plants by altering the (functional)
CC level in the plant cells of a cell-division controlling protein that can
CC bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin.
CC Modulation of the cyclin gene is used to increase or decrease the growth
CC rate, provide faster germination, reduce time to flowering, increase the
CC number of flowers, seeds or fruits per plant, increase root development,
CC reduce height and to delay flowering in a range of plants, e.g. legumes,
CC grasses, maize, oilseed rape, wheat, tomato, rice, barley, sunflower,
CC carnation, chrysanthemum, rose, tulip, etc.
XX
SQ Sequence 1846 BP; 448 A; 425 C; 514 G; 458 T; 1 other;
XX
XX
alignment_scores:
Quality: 621.50 Length: 356
Ratio: 2.762 Gaps: 10
Percent Similarity: 63.202 Percent Identity: 39.888
XX
alignment_block:
US-09-530-209A-2 x AAV33889
XX
Align seq 1/1 to: AAV33889 from: 1 to: 1846
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   |||||.....||| :||| |||||.....|||
349 CTGCTGTGCGCGGAGCAACGCTGATTTCTGCGCTGAGCAGCATGG 398
   :||| :||| ||| :|||.....|||
21 ymet..... 22
   :||| :||| ||| :|||.....|||
399 GGAAGAGTCTCTGTGGCGCGCGCTACGCCCACTGACACCGTGC 448
   :||| :||| ||| :|||.....|||
23 .....lleValAspGlnThr 27
   :||| :||| ||| :|||.....|||
449 CCGCCGCCCGCCGACCGGGGTGCGCGTGCATGGGATTTTGCAGGATTC 498
   :||| :||| ||| :|||.....|||
28 ProileGlnleSerileProGlnMetGlyPheSerGlnSerGlnSerG1 44
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499 CCCTTG.....CTCTCGGA 512

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61 spsptylrilelserglau.....ArgSerCylspleuasn 75
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563 AGGGGTACTCCGAAGCTGCACGACGCGCATGGGACCTGGATTGGCC 612
76 valgllyargargspalaleuasntrpilletrpilalacysgluvalhi 92
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613 GCCGTGAGAGAGAGCGCATCGATTGATTTGGAGATTCATTGACATTA 662
92 sglnphleglproleucysphecysleualametasntryleuaspargp 109
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663 CAATTTCGACCGCTTGACTGCCGTTTGTCTGTGACTACTCTGCATAGAT 712
109 heluSerValHlsaspLeuProSerCylslyslYtrpilleuGlnleu 125
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
713 TCCTCTCAGATAGAGTTCCTGAAAGCAGAGCTTGATGACTCAGCTC 762
126 leualalalalacysleuSerleualalalalyslleuglnthrGluA 142
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
763 TTGGCACTGGCTTGTCTTGTCTTGGCTTCGAAATCGAAGACTTTGT 812
142 lProMetleuHlsaspLeuGlnValglYaspProGlnPheValPheGluA 159
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813 GCCACTCCCTTGATTTGCGAGTAGCGGAGCGCAAGTTGTTTGTAGG 862
159 lalysSerValGlnArgmetGluLeuValleuasnlyslleuYsTrp 175
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
863 GAAGGACCAATAAAAGATGAGCTTGCTGAGCTAGACACTTAAAGTGG 912
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913 AGGATGCACTGCTTACTGCTGCTCATTTGTGAATACTTTCTTCAATA 962
192 smetserlyscysaspGlnleuProSerAsnThrleuIleSerArgserL 209
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
963 ATTGAGTAT...CATGCTGACCCCTCTGCTTGCACGCTCTGCTCTT 1009
209 euglnValIleAlaSerThrThrlysglylleaspPheleuGluPheArg 225
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1010 CGGACCTTGTCTTGAGCACCCGCTAAGTGTGATTTGTTGATTCAGA 1059
226 ProSerGluAlaAlaAlaAlaValaleuSerValSerGlyGluLeuG1 242
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1060 CCTCCGAGATTGCTGCCAGTGTGACTGCTGCTATCGGCGAATGCAG 1109
242 nArgValHlsPheaspasnSerSerPheSerProleuPheSerleuLeug 259
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1110 GAGTCTGTGAATGAGAGAGCTGAGTAGCTGCAAAAT...TTGG 1153
259 lnlYsgluArgValYalyslysllleglylumeIleGlu..... 271
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1154 ACAAGGAGAGGGTTTAAAGATCCATGAATGATTCAGAGAGAATTA 1203
272 .....SeraspGlySeraspLeuCysSer..... 279
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1204 GCGGGAAGCATGTGCTTAAGTCTGCTGATCATCAATCTCCTGTGTGCC 1253
280 glnthrProasnGlyValleuGluValSerAlaCys..... 291
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::
1254 ACAAAAGCCCAATAGTGTCTGAGACCTGACCTGTGATCAACAAA 1303
292 .....CysPheSerPheYsThr 297
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1304 GCGATGACCTACTGTGCGGCTCTCTGAGTATGTTAC..... 1341
298 HlsaspSerSerSerSer 303
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1342 CATAGTTCTTCCACAAGC 1359

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seq_name: /SIDS2/gcycdata/geneseq/geneseqn/MA2000.DAT:AA294581
seq_documentation_block:
ID AA294581 standard; DNA: 1861 BP.
XX
AC AA294581;
XX
DT 18-JUL-2000 (first entry)
XX
DE Maize cyclin D ZmCycD gene.
XX
KW Maize; cyclin D; ZmCycD gene; CycD; cell division; cell cycle;
transgenic plant; ss.
XX
OS Zea mays.
XX
FH Key Location/Qualifiers
FT CDS 275..1351
FT /tag= a
XX
XX MO200017364-A2.
XX
XX 30-MAR-2000.
XX
XX 21-SEP-1999; 99WO-US21946.
XX
XX 23-SEP-1998; 98US-0101551.
XX
XX (P10N-) PIONEER HI-BRED INT INC.
XX
XX Lowe KS, Tao Y, Gordon-Kamm WJ, Gregory CA, McElver JA;
XX Hoester GJ;
XX
XX WPI: 2000-283589/24.
XX P-PSDB: AAY79321.
XX
XX Novel polynucleotides encoding maize cyclin D isoforms 1, 2 and 3,
XX related proteins and antisense RNA useful for control of cell cycle
XX regulation
XX
XX Claim 1; Page 115-117; 134pp; English.
XX
XX The present sequence is that of an isoform of the maize ZmCycD
XX gene that encodes cyclin D (CycD, see AAY79321), a protein necessary
XX for progression from G1 into S phase. The encoded protein binds to
XX CDK4, and the active CycD-CDK4 hyperphosphorylates retinoblastoma
XX associated protein, releasing the E2F transcription factor which
XX activates DNA synthesis. The invention provides maize CycD
XX polynucleotides (see AA294581-84) and polypeptides (see AAY79321-24)
XX that are involved in cell cycle regulation. Also provided are
XX recombinant expression cassettes (including ZmCycD in sense or
XX antisense orientation), host cells, transgenic plants (especially
XX corn, sorghum, sunflower, safflower, wheat, rice, alfalfa or
XX oilseed Brassica) and antibody compositions. A claimed method of
XX modulating the level of CycD protein in a cell comprises
XX transforming the cell with a recombinant expression cassette
XX comprising a CycD polynucleotide linked to a promoter, and
XX growing the cell for a time sufficient to induce expression of the
XX polynucleotide sufficient to modulate (increase or decrease) the
XX CycD protein in the cell. The CycD protein is present in an amount
XX sufficient to alter cell division, increase the number of cells
XX dividing, improve transformation frequencies, alter cell growth,
XX increase the growth rate, increase crop yield, alter plant
XX height or size, enhance or inhibit organ (seed, root, shoot, ear,
XX tassel, stalk, pollen, stamen) growth, produce organ ablation,
XX produce parthenocarpic fruits, produce male sterile plants,
XX enhance embryogenic response, increase callus induction, provide
XX positive selection, increase plant regeneration, alter the time
XX that cells are arrested in G1 or G0 phase or in a particular cell
XX cycle, improve response to environmental stress including
XX dehydration, heat or cold, increase the number of pods per plant,
XX increase the number of seeds per pod or ear, alter the lag time in
XX seed development, provide hormone-independent cell growth, or

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CC Increase the growth rate of cells in bioreactors. The level of
CC CycD protein in the cells is transiently modulated by introducing
CC CycD RNA or CycD polypeptides. CycD polynucleotides can be used
CC to identify CycD interacting proteins. All claimed.

XX Sequence 1861 BP; 462 A; 413 C; 512 G; 474 T; 0 other:

alignment_scores:

Quality:	621.50	Length:	356
Ratio:	2.762	Gaps:	10
Percent Similarity:	63.202	Percent Identity:	39.888

alignment_block:

us-09-530-209a-2 x AA294581

Align seg 1/1 to: AA294581 from: 1 to: 1861

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10 LeuLeuCythrGluSerAsn.....ValAspAspGluG1 21
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   21 yMet.....
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   23 .....
408 CCGCCCGCCGCCGACCGGGGTCGCCGTCGATGATTTTGACGGAGATTC 457
   |||||.....
28 ProIleGluLeuSerIleProGlnMetGlyPheSerGlnSerGluSerG1 44
   |||||.....
458 CCCTTG.....CTCTCGGA 471
44 uGluIleIleMetGluMetValGluGluGluGlnHisIleuProSerA 61
   |||||.....
472 TGACGTGGGTGGCAGCCTCTGCGAAGAGAGTGACGACATGCCCCGG 521
   61 spAspIlyrIleLysArgLeu.....ArgSerGlyAspLeuAsn 75
   |||||.....
522 AGGGGATACCTCCAGAACGTCACGACGATGGGGCTGATTTGGCC 571
   76 ValGlyArgArgAspAlaLeuAsnTrpIleTrpLysAlaCysGluValH1 92
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572 GCCGTGAGAGAGAGCCGATGATTTGGAAGGTCAATTGACCTTA 621
   92 sGlnPheGlyProLeuCySpheCysLeuAlaMetAsnTrpLeuAspArg 109
   |||||.....
622 CAATTTCGACCGCTTGACTGCCGTTTGTCTGTAACCTGATGATGAT 671
   109 heLeuSerValHisAspLeuProSerGlyLysGlyTrpIleLeuGlnLeu 125
   |||||.....
672 TCCTCTCCAGATGATGATCCCTGAAAGGAGAGTGGATGACACATC 721
   126 LeuAlaValAlaCysLeuSerLeuAlaAlaLysIleGluGlnTrpGluVal 142
   |||||.....
722 TTGGCACTGCTGCTTGTCTTTGGCTTGCAGAAATCGAAGAGACTTTGT 771
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   159 lAlysSerValGlnArgMetGluLeuValLeuAsnLysLeuLysTrp 175
   |||||.....
822 GAAGGACCAATAAAAAGATGAGCTTCTGCTCAACACCTTAAAGTGC 871
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   |||||.....
872 AGGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 921
   192 smetSerLysCysAspGlnGluProSerAsnTrpLeuIleSerArgSerL 209
   |||||.....
922 ATTAGAGTAT...CATGTGACACCTCTGCTTGCACGCTCTGCTGCTT 968

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```

209 eugHnValIleAlaSerThrThryLysGlyIleAspPheLeuGluPheArg 225
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   |||||.....
1019 CCTCCGAGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1068
   242 nArgValHisPheAspAsnSerSerPheSerProLeuPheSerLeuLeu 259
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1069 GAGTTCGTATATGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1112
   259 lnyLysGluArgValLysLysIleGlyLysMetIleGlu..... 271
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   |||||.....
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1263 GCGATGACGCTACTGTCGGGCTCTCTGCTGATGATTTAC..... 1300
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seq_documentation_block:
ID AA294582 strand: DNA; 1077 BP.
XX
AC AA294582:
XX
DT 18-JUL-2000 (first entry)
XX
DE Maize cyclin D zmcycd gene.
XX
KW Maize; cyclin D; zmcycd gene; CycD; cell division; cell cycle;
XX transgenic plant; ss.
XX
OS Zea mays.
XX
PN WO200017364-A2.
XX
PD 30-MAR-2000.
XX
PF 21-SEP-1999; 99WO-US21946.
XX
PR 23-SEP-1998; 98US-0101551.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Lowe KS, Tao Y, Gordon-Kamm WJ, Gregory CA, McEliver JA;
XX Hoerster GJ;
XX WPI; 2000-283589/24.
XX P-PSDB; AAT79322.
XX
PT Novel polynucleotides encoding maize cyclin D isoforms 1, 2 and 3,
XX related proteins and antisense RNA useful for control of cell cycle
XX regulation
XX
PS Claim 1, Page 120-121; 134pp; English.
XX
CC The present sequence is that of an isoform of the maize zmcycd
XX gene that encodes cyclin D (CycD, see AAT79322), a protein necessary

```

76 ValGIvArqArqAspAlaLeuAsnTriPleTTrpLysAlaCysGluValHi 9

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299	GCCTGTCAGGAAGACCCGATCGATTTGGATTTCGAAGCGTCATTCGAGCATTA	347
92	sglnPheGlyProLeuCySPheCySPheLysLeuAlaMetAsnTyrlLeuAspArg	109
348	CAATTTGGACCGCTTGGACTGCCGTTTTCCTCTGTGTGAACCTACCTCGATAGT	397
109	heLeuSerValHisAspLeuProSerGlyLysGlyTyrPrlLeuGlnLeu	125
398	TCCCTCCACGATGATGATTCCTCGAAGGACAGAGCTTGATGACTCGATC	447
126	LeuAlaValAlaCySPheLeuSerLeuAlaAlaLysIleGlnGlnThrCluVal	142
448	TTGGCAGAGCGCTTGGCTTCTTTGGCTTCGAAATCGAAGAGACTTTTGT	497
142	lPrometLeuIleAspLeuGlnValGlyAspProGlnPheValPheGlyua	159
498	GCCACTCCCTTCGTGATTTGGACGTACGCGAGCGACCAAGTTGTTTGGAG	547
159	lAlYSerValGlnArgMetGlnLeuLeuValLeuAsnLysLeuLysTyr	175
548	GAAGGACCATTAAGAGATGAGAGCTTCCTGCTCTTAAGCACTTAAGGTG	597
176	ArgLeuArgAlaIleThrProCysSerTyrIleArgTyrPheLeuArgly	192
598	AGGATGATCGCTTACTGCTGCTGCTCATTTGTGAACTACTTTTTCATA	647
192	smetSerLysCysAspGlnGluProSerAsnThrLeuIleSerArgSerL	209
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XX	18-JUL-2000 (first entry)	
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XX	Maize cyclin D ZmCycd gene.	
XX		

KW Maize: cyclin D; ZmCYCD gene; CycD; cell division; cell cycle;
 KW transgenic plant; ss.
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 PD 30-MAR-2000.
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 PF 21-SEP-1999; 99WO-US21946.
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 PR 23-SEP-1998; 98US-0101551.
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 PA (PION-) PIONEER HI-BRED INT INC.
 XX
 PI Lowe KS, Tao Y, Gordon-Kamm WJ, Gregory CA, McElver JA;
 PI Hoerster GJ;
 DR WPI: 2000-283589/24.
 DR P-PSDB; AA799323.
 XX
 PT Novel polynucleotides encoding maize cyclin D isoforms 1, 2 and 3,
 PT related proteins and antisense RNA useful for control of cell cycle
 PT regulation -
 XX
 PS Claim 1: Page 122-124; 134pp; English.

The present sequence is that of an isoform of the maize ZmCYCD gene that encodes cyclin D (CycD, see AA799323), a protein necessary for progression from G1 into S phase. The encoded protein binds to CDK4, and the active CycD-CDK4 hyperphosphorylates retinoblastoma associated protein, releasing the E2F transcription factor which activates DNA synthesis. The invention provides maize CycD polynucleotides (see AA794581-84) and polypeptides (see AA79321-24) that are involved in cell cycle regulation. Also provided are recombinant expression cassettes (including ZmCYCD in sense or antisense orientation), host cells, transgenic plants (especially corn, sorghum, sunflower, safflower, wheat, rice, alfalfa or oilseed Brassica) and antibody compositions. A claimed method of modulating the level of CycD protein in a cell comprises transforming the cell with a recombinant expression cassette comprising a CycD polynucleotide linked to a promoter, and growing the cell for a time sufficient to induce expression of the polynucleotide sufficient to modulate (increase or decrease) the CycD protein in the cell. The CycD protein is present in an amount sufficient to alter cell division, increase the number of cells dividing, improve transformation frequencies, alter cell growth, increase the growth rate, increase crop yield, alter plant height or size, enhance or inhibit organ (seed, root, shoot, ear, tassel, stalk, pollen, stamen) growth, produce organ ablation, produce parthenocarpic fruits, produce male sterile plants, enhance embryogenic response, increase callus induction, provide positive selection, increase plant regeneration, alter the time that cells are arrested in G1 or G0 phase or in a particular cell cycle, improve response to environmental stress including dehydration, heat or cold, increase the number of pods per plant, increase the number of seeds per pod or ear, alter the lag time in seed development, provide hormone-independent cell growth, or increase the growth rate of cells in bioreactors. The level of CycD protein in the cells is transiently modulated by introducing CycD RNA or CycD polypeptides. CycD polynucleotides can be used to identify CycD interacting proteins. All claimed.

Sequence 1173 BP; 200 A; 366 C; 416 G; 191 T; 0 other:

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KM protein identification; signal transduction pathway;
KM metabolic pathway; promoter; termination sequence; ss.
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KM   CDC; RP; retinoblastoma; germination; flowering; seed; fruit;
KM   root development; ds.
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PM   W09842851-A1.
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PD   01-OCT-1998.
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PF   24-MAR-1998; 98MO-EP01701.
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PA   (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
PI   Murray JAH.
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DR   WPI; 1998-532012/45.
XX
PT   Regulating growth and structure of plants by modulating protein that
PT   controls cell division - specifically a D-type cyclin, and related
PT   chimeric genes and transformed cells and plants, used to alter
PT   growth rate, flowering, seed production etc.
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PS   Claim 14; p56-57; 75pp; English.
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CC   This sequence represents the CYCD1;1 cDNA from Helianthus tuberosus which
CC   encodes a D-type cyclin. The sequence can be used to alter the growth
CC   characteristics or architecture of plants by altering the (functional)
CC   level in the plant cells of a cell-division controlling protein that can
CC   bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin.
CC   Modulation of the cyclin gene is used to increase or decrease the growth
CC   rate, provide faster germination, reduce time to flowering, increase the
CC   number of flowers, seeds or fruits per plant, increase root development,
CC   reduce height and to delay flowering in a range of plants, e.g. legumes,
CC   grasses, maize, oilseed rape, wheat, tomato, rice, barley, sunflower,
CC   carnation, chrysanthemum, rose, tulip, etc.
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XX 21-DEC-1999 (first entry)

XX Soybean cyclin delta-1 cDNA.

XX Cyclin delta-1; soybean; cell cycle; cell division;

XX transgenic plant; herbicide; plant breeding; ss.

XX Glycine max.

XX Key Location/Qualifiers

XX FT CDS 1..957

XX FT /*tag= a

XX PN MO9948486-A2.

XX PD 30-SEP-1999.

XX PF 19-MAR-1999; 99WO-US06047.

XX PR 23-MAR-1998; 98US-0078948.

XX PA (DDPO) DU PONT DE NEMOURS & CO E. I.

XX PI Caboon RE, Klein TM, Odell JT, Orozco EM;

XX DR MPI: 1999-591036/50.

XX DR P-PSDB: AA231895.

XX PS Claim 7; Page 53-54; 68pp; English.

XX CC This nucleotide sequence represents a portion of the cDNA insert in

XX CC clone seg.ph0028.f11 encoding a portion (see AA231895) of a soybean

XX CC cyclin delta-1 protein. The clone was isolated from a soybean

XX CC embryo (26 days after flowering) cDNA library. The invention

XX CC relates to isolated nucleic acid fragments (see AA219953-66)

XX CC encoding cyclin A, cyclin delta-1, cyclin delta-2 and cyclin delta-3

XX CC polypeptides (see AA231889-902). It also relates to the construction

XX CC of chimeric genes encoding all or a portion of a cyclin, in sense

XX CC or antisense orientation, where expression of the chimeric gene

XX CC results in altered levels of the cyclin protein in a transformed

XX CC host cell. This would have the effect of altering the regulation

XX CC of cell division in those cells. The nucleic acid fragments may be

XX CC used to express cyclins in plant cells to enhance cell tissue

XX CC culture growth. The availability of nucleic acid sequences encoding

XX CC all or a portion of cyclins should facilitate studies of cell cycle

XX CC in plants, provide genetic tools to enhance cell growth in tissue

XX CC culture, increase the efficiency of gene transfer and help provide

XX CC more stable transformations. The proteins can be used as targets

XX CC to facilitate design and/or identification of inhibitors of those

XX CC enzymes that may be useful as herbicides.

SO Sequence 1994 BP; 534 A; 361 C; 477 G; 622 T; 0 other;

alignment_scores:

Quality: 402.00 Length: 313

Ratio: 2.116 Gaps: 9

Percent Similarity: 60.703 Percent Identity: 35.783

alignment_block:

US-09-530-209a-2 x AA219959

Align seg 1/1 to: AA219959 from: 1 to: 1994

23 lleValaspluThrProIleGluIleSerIleProGlnmetGlyPhe 39
 |||:||||:||||| ||| |||
 13 ATCATGATTCCTCGCGG...GAGTGTCTCTCGAGCTCATTCCTCGCC 59
 39 rgInSerGluSerGluGluIleIleMetGluMetValGluLysGlu 56
 |||||:||||: ||| |||
 60 GCCGTGCGAGCGGAGTCC...ATCGCGGATTCATGAGACGACGCGCA 106
 56 InhlSerProSerAspAspTyrIleLysArgLeuArgSerGlyAsp 72
 :|||:||||: ||| |||
 107 ACTTCGTCGCCGATTCGAATTCCTCAATAGTTCATTCGCTCTCTC 156
 73 AspleuAnValGlyArgAspAlaLeuAnThrIleTrpIleValAla 89
 ||| :|||:||||: ||| |||
 157 GACGCTCT...GCCAGAGAGATCCGTTGCATGATTCCTCAAGTGA 203
 89 sGluValHisGlnPheGlyProLeuCySphCySphCySphCySph 106
 :||| :|||:||||: ||| |||
 204 GCGTATTACGCTTTTCACCGGTCACGCGCTTATCTTCGTTAACTACT 253
 106 euAspArgPheLeuSerValHisAspLeu...ProSerGlyLysGly 121
 |||||:||||: ||| |||
 254 TGCTAGGTTCTTGAATTCGACCGCTTCCGCGGAAAGGAGGCTG 303
 122 lleuGlnleuLeuAlaValAlaCysLeuSerLeuAlaLysIleG 138
 |||||:||||: ||| |||
 304 CCACTGCACTTCTCTGCTTGGCTGCTTGTCTTACGACGAAAGATGA 353
 138 uGluThrGluValProMetLeuIleAspLeuGlnValGlyAspPro 155
 |||||:||||: ||| |||
 354 GAATCTCTAGTTCATCTCTTGGACCTTACGCTGAAGGCTCAAT 403
 155 heValPheGluAlaLysSerValGlnArgMetGluLeuValLeuAs 171
 :|||:||||: ||| |||
 404 ACCTATTGGAACCCCAACCAATTAAGAGAGACCTGCTCTGCGC 453
 172 LysLeuLysTrpArgLeuArgAlaIleThrProCysSerTyrIle 188
 ||| |||||:||||: ||| |||
 454 GTGTTGATTTGAGGCTAAGATCGTTACCCATTTACCTTCGATTT 503
 188 rPheLeuArgLysMetSerLysCySAspGlnGluProSerAnThr 203
 :||| :|||:||||: ||| |||
 504 CTTT...GCGTCAAGTTAGATTCACAGCTGACCTTTTA 538
 204LeuIleSerArgSerLeuGlnValIleIleAspThrLys 217
 |||||:||||: ||| |||
 539 CCGGTTCTCATTTTCAGTGTACACCAATTAATTAATTAATTA 588
 218 GlyLeuAspPheLeuGluPheArgProSerGluValAlaIleVal 234
 :|||:||||: ||| |||
 589 GAGCTAGCTTTCTTGGCTATGTCATCATGATTCGTGACGACCAT 638
 234 aleuSerValSerGlyLeuGlnArgValHisPheAspAnSerSer 251
 ||| :|||:||||: ||| |||
 639 TCTCCATGACCAATGAATTT... 660
 251 heSerProLeuPheSerLeu... 257
 :||| :|||:||||: ||| |||
 661 ...CCTAATGCTCTCTGTTAGCGCTGACATGACAGCTCATGCTGT 705
 258LeuGlnLysGluArgValLysLysIleGlyGluMetIleG 272
 |||||:||||: ||| |||
 706 GAGCGTTAGCAAGCAAAATATATAGCGCTACCAATTAATGACAGA 755
 272 rAspGlySerAspLeuCySserGlnThrProAsnGlyValLeuGlu 287
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292 ysphsePheIysThriIsasPseSerSerTyThriIsleuSer 308
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 1153 GCGACAG.....TCTATGATTCGTGCTCGTACATCTTCATTTC 1196

[illegible]

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GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,772
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1970 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 22..948
US-08-463-772-3

alignment_scores:
Quality: 240.50 Length: 298
Ratio: 1.286 Gaps: 15
Percent Similarity: 62.752 Percent Identity: 29.530

alignment_block:
US-09-530-209A-2 x US-08-463-772-3 ..

Align seg 1/1 to: US-08-463-772-3 from: 1 to: 1970

6 leudluenseurleuencysThrGluserAsn.....Va 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
16 TTGGCCATGGAGAGCTGCTGTGCACAGAGGAGACCCGGTCCGACGAGCCCT 65
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17 LASPAspIuGljMeliIevaLaspIuThrProIleGluIleSerIleP 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
66 GCGGAGCCGCAACCTGCTCGAGACGACGACCGCGCTCTCGAG...AACCTCG 112
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 roGImetGlyPheSerGlnSerGlnSerGlnGluIleIle.....47
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
113 TCACCATCGAAATTCCCGCGCGGCGCTTGGCCATGAGCTGCTGTCCACAG 162
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
48 MetGluMetValGluGluIuysGluIuysGlnHisLeuProSerAspAspTyr11 64
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
163 GGGAGCCCGCGTCCGACGAGGAGAGCGGCTACGTTCCGACAGTGCCTACTT 212

```

[illegible][illegible]

```

TELEFAX: (215) 568-5549
TELEX: No. 5734039E
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 1325 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-306-691B-51

alignment_scores:
Quality: 240.00 Length: 288
Ratio: 1.379 Gaps: 11
Percent Similarity: 60.417 Percent Identity: 29.167

alignment_block:
US-09-530-209A-2 x US-08-306-691B-51 ..

Align seg 1/1 to: US-08-306-691B-51 from: 1 to: 1325

6 LeuGIuLeuSerLeuLeuCysThrGluSerAsnValAspAspGluIglye 22
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145 ATGAACACCAGCCTCGTGTGGAAATG..... 174

22 ttleValaspGluThrProIleGluIleSerIleProIleMetGlyPheS 39
:::|||| |:::| |:::| |:::|
175 ..... GAACCC...ATCCCCCGCGCTACCCCATGCCAACCTCC 211
:::|:::| |:::| |:::| |:::|
39 engInserGluSerGluGluIleIleMetGluMetValGluLysGluYs 55
:::|:::| |:::| |:::| |:::|
212 TC..... AACGACCGGTCGTGC CGCGCGCATCTGAAGCGGAGAG 252
:::|:::| |:::| |:::| |:::|
56 GluHisLeuProSerAspPtyrIleLysArgLeuAspSerGlyAlaPse 72
||||| |:::| |:::| |:::| |:::|
253 ACCTGCGCGCGCTCGTGTCCTACTCAAAATGTGTGCAGAAGAGAGTCT 302
||||| |:::| |:::| |:::| |:::|
72 uAspLeuAsnValGlyArgArgAspAlaLeuAsnTrpIleTrpLysAlaC 89
|:::| |:::| |:::| |:::| |:::|
303 GCCGTCATG.... CGAAGATCCTGCCACACCTGATGTCGAGAGTCT 346
|:::| |:::| |:::| |:::| |:::|
89 ysgIuValHisGlnPheGlyProLeuCysPheCysLeuAlaMetLsnTr 105
||||| |:::| |:::| |:::| |:::|
347 GCGGAGAACAAGATGCGAGAGAGAGTCTTCCCCTGCCCATGAACCTAC 396
||||| |:::| |:::| |:::| |:::|
106 LeuAspArgPheLeuSerValHisAspLeuProSerGlyLysGlyTyrIl 122
||||| |:::| |:::| |:::| |:::|
397 CTGACCGCTTCGTGCTGCTGAGCCCTGAAAAAGAGCCG..... 438
||||| |:::| |:::| |:::| |:::|
122 eLeuGlnLeuLeuAlaValAlaCysLeuSerLeuAlaAlaLysIleGlu 139
||||| |:::| |:::| |:::| |:::|
439 .CTGCAGCTGCTGGGGCGCACCTTCATGCTTCTGCCTTAAGATCAAG 487
||||| |:::| |:::| |:::| |:::|
139 LuThrGluValPrometLeuIleAspLeuGlnValGlyAspProGlnPhe 155
||||| |:::| |:::| |:::| |:::|
488 AGACC..ATCCCCCTGACGCGCCGGAACCTGTGATCTACACCGCAGGC 534
||||| |:::| |:::| |:::| |:::|
156 ValPheGluAlaLysSerValGlnArgMetGluLeuLeuValLeuAsnLy 172
:::|:::| |:::| |:::| |:::| |:::|
535 TCCATCCGCGCCCGAAGAGTCTGCAAAATGAGAGCTCTCTGTTGAACAA 584
:::|:::| |:::| |:::| |:::| |:::|
172 sLeuLysTrpArgLeuArgAlaIleThrProCysSerTrpIleArgTyr 189
||||| |:::| |:::| |:::| |:::|
585 GCTCAAGGGAACCTGGCGCGCATACCCCGACAGATTTCATTGAAACACT 634
||||| |:::| |:::| |:::| |:::|
189 heLeuArgLysMetSerLysCysAspGlnGluProSerAsnThrLeuile 205
||||| |:::| |:::| |:::| |:::|
635 TCCTCTCCAAAATGCCA..... GAGCGGAGAGAGAACAAACAGATCATC 678
||||| |:::| |:::| |:::| |:::|
206 SerArgSerLeuGlnVal...lleAlaSerThrThrLysGlyIleAspPh 221
:::|:::| |:::| |:::| |:::| |:::|
679 GCCAAAACAGCGCGAAGACTTCTGTCCTTGTGGCCACAGATGTGAAGTT 728

```



```

ADDRESS: Leona L. Lauder
STREET: Stewart Street Tower, 18th Fl., One Market
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,893A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/947,120
FILING DATE: 17-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: 91-210-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-777-9257
TELEFAX: 415-543-4219
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4221 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHEICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 142..1026
US-08-472-893A-7

alignment_scores:
Quality: 236.00      Length: 293
Ratio: 1.349        Gaps: 13
Percent Similarity: 59.727      Percent Identity: 28.669

alignment_block:
US-09-530-209A-2 x US-08-472-893A-7
Align seg 1/1 to: US-08-472-893A-7 from: 1 to: 4221

6 LeuGluLeuSerLeuLeuGlyThrGluSerAsnValAlaAspGluGlyMe 22
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142 ATGCAACACACAGCTCTGCTGCGAAGTC..... 171
22 tLeValAspGluThrProIleGluIleSerIleProGluMetGlyPheS 39
   ::::: ::::: ::::: :::::
172 .....GAAACC...ATCCGCGCGCGCTACCCGATGCCAAGCTCC 208
39 erGlnSerGluSerGluGluIleIleMetGluMetValGluGlyGluLys 55
   ::::: ::::: ::::: :::::
209 TC.....AACGACCGGCTGCTCGGCGCCATGTCGAAGCGGAGAG 249
55 GlnHisLeuProSerAspAspTyrIleLysArgLeuArgSerGlyAspLe 72
   ::::: ::::: ::::: :::::
250 ACCTGCGCGCGCTGCTGCTCTACTTCAATGTGTGCAAGAGAGTCTT 299
72 uAspLeuAsnValGlyArgArgAspAlaLeuAsnTrpIleTyrPylalac 89
   ::::: ::::: ::::: :::::
300 GCCGCTCCATG.....CGAAGATCTGCGCCACCTGGATCTGTGAGGTCT 343
89 ysgLValHisGlnPheGlyProLeuGlyPheCysLeuAlaMetAsnTyr 105
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344 CGAGGAAACAGAACTGGAGAGAGAGGTCTTCCCGCTGCGCATGAACACTAC 393

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106 LeuAspArgPheLeuSerValHisAspLeuProSerGlyLysGlyTrpIle 122
   ::::: ::::: ::::: :::::
394 CTGACCGCTTCTCTGCTGAGACCCGTGAAAAAGCGCC..... 435
122 eLeuGlnLeuValAlaValAlaCysLeuSerLeuAlaAlaLysIleGlu 139
   ::::: ::::: ::::: :::::
436 .CTGCAGCTCTGCGGCGCCACTGATGTTCTGCGCTCTTAATGAGAG 484
139 luthrGluValProMetLeuIleAspLeuGlnValGlyAspProGlnPhe 155
   ::::: ::::: ::::: :::::
485 AGACC...ATCCCCCTG.....ACGCGGAGAGCTGTGTC 516
156 ValPheGluAlaLysSerValGln.....ArgMetGluLe 167
   ::::: ::::: ::::: :::::
517 ATCTACACCGCAACTCTCATCCGCGGAGAGCTGCTGCAAAATGAGCT 566
167 uLeuValLeuAsnLysLeuLysTrpArgLeuArgAlaIleThrProCys 184
   ::::: ::::: ::::: :::::
567 GCTCTGCTGTAACAGCTCAAGTGGAACCTGCGCGCAATACCCCGCAGC 616
184 erTyrIleArgTyrPheLeuArgLysMetSerLysCysAspGlnGluPro 200
   ::::: ::::: ::::: :::::
617 ATTTCATGAACACTCTCTCCAAATGCCA.....GAGCGGAGAG 660
201 SerAsnThrLeuIleSerArgSerLeuGlnVal...IleAlaSerThr 216
   ::::: ::::: ::::: :::::
661 AACAAACAGATCATCCGCAACACGCGGAGAGCTGCTGCTGCTGTC 710
216 rLysGlyIleAspPheLeuGluPheArgProSer...GluAlaAlaIle 232
   ::::: ::::: ::::: :::::
711 CACAGATGTAAGTTCATTTCATCCGCGCTCTCATGTGGACGCGGGA 760
232 lAValAlaLeuSerValSerGlyGluLeuGlnArgValHisPheAspAsn 248
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761 GCGTGTGCGCGCAGTCAGAGCGCTGAACCTGAG..... 795
249 SerSerPheSerProLeuPheSerLeuLeuGlnLysGluArgValLys 265
   ::::: ::::: ::::: :::::
796 .....AGCCCAACAACTTCTGCTCTACTACCGCTCAACGCTT 836
265 sIleGlyLysMetIleGluSerAspGlySerAspLeu.....CysSerG 280
   ::::: ::::: ::::: :::::
837 CCTCTCCAGATGATCAAGTGTGACCCGCGACTGCTCGGCGCTGCCAGG 886
280 lnthrProAsnGlyValLeuGluValSer 289
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887 AGCAGATCAAGACCTCTGATGATCAAGC 915

seq_name: /cgn2_6/ptodata/2/lna/6A_COMB.seq:US-08-947-492-7
seq_documentation_block:
: Sequence 7, Application us/08947492
: Patent No. 6127118
: GENERAL INFORMATION:
: APPLICANT: Meeker, Timothy C.
: TITLE OF INVENTION: BCI-1 Locus Nucleic Acid Probes and
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Leona L. Lauder
: STREET: Stewart Street Tower, 18th Fl., One Market
: CITY: San Francisco
: STATE: CA
: COUNTRY: USA
: ZIP: 94105
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/947,492
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/472,893
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: 91-210-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-777-9257
TELEFAX: 415-543-4219
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4221 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 142..1026
US-08-947-492-7

alignment_scores:
Quality: 236.00 Length: 293
Ratio: 1.349 Gaps: 13
Percent Similarity: 59.727 Percent Identity: 28.669

alignment_block:
US-09-530-209a-2 x US-08-947-492-7 ..

Align seg 1/1 to: US-08-947-492-7 from: 1 to: 4221

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6 LeuGlulSerLeuLeuSerLeuGluSerLeuValAspValAspGluGlyme 22
142 ATGGAAACACCACTCTGCTGCTGCGAAGTG..... 171
22 ttleValAspGluThrProIleGluIleSerIleProGluMetGlyPhe 39
172 .....GAAACC...ATCCGGCGCGGTACCCGATGCCAAGCTCC 208
39 erGlnSerGluSerGluIleIleMetGluMetValGluGlyGluGly 55
209 TC.....AACGACCGGGTCTGCGGCGCATGCTGAAGCGCGAGAG 249
56 GlnHisLeuProSerAspTyrIleLeuArgLeuArgSerGlyAspLe 72
250 ACCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 299
72 uAspLeuAsnValGlyArgArgAspAlaLeuAsnTyrIleTyrPhe 89
300 GCGGTTCATG.....CGAAGATCGTCGCGACCTGATGCTGAGAGTCT 343
89 yGluValHisGlnPheGlyProLeuGlyPheGlySerLeuAlaMetAsnTyr 105
344 GCGAGGAAACGAGAGTGTGCGGAGAGAGTCTCCGCTGCGCATGAACTAC 393
106 LeuAspArgPheLeuSerValHisAspLeuProSerGlyIleGlyTyrP 122
394 CTGAGACCGCTTCTGCTGCTGCGACCCGCTGAAAAAGACCCG..... 435
122 eleuGlnLeuLeuAlaValAlaCysLeuSerLeuAlaAlaIleGluG 139
436 CTGACACTCTGCGGCGCACTTCATGCTGCTGCTGCTGCTGCTGCTG 484
139 luthrGluValProMetLeuIleAspLeuGlnValGlyAspProGlnPhe 155
485 AGACC...ATCCCCCTG.....ACGGCCGAGAAAGCTGTGC 516
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156 ValPheGluAlaLysSerValGln.....ArgMetGluLe 167
517 ATCTACACCGACCACTTCATCCGGCCGAGAGACTCTCTCAATGAGCT 566
167 uLeuValLeuAsnLysLeuLysTyrArgLeuArgAlaIleThrProCys 184
567 GCTCTGTGTGACCAAGCTCAAGTGAAGTGGCGGCAATGACCCGACAG 616
184 erTyrIleArgTyrPheLeuArgLysMetSerLysCysAspGlnPro 200
617 ATTTCATGTAAACCTTCCTCCAAATGCCA.....GAGCGGAGAG 660
201 SerAsnThrLeuIleSerArgSerLeuGlnVal...IleAlaSerThr 216
661 ACAAAACAGATATCCGCAAAACGCGCAGACCTTGCTGCTGCTGCTG 710
216 rLysGlyIleAspPheLeuGlnPheArgProSer...GluAlaAla 232
711 CACAGATGTGAAGTTCATTCCAATCCGCCCTCCATGCTGCGAGCGGA 760
232 lValAlaLeuSerValSerGlyLeuGlnArgValHisPheAspAsn 248
761 GCCTGTGTGCGCGCAGTGCAGAGGCTGAACCTGAG..... 795
249 SerSerPheSerProLeuPheSerLeuGlnLysGluArgValLys 265
796 .....AGCCCAACAACTTCCTGCTGCTGCTGCTGCTGCTGCTG 836
265 sileGlyGluMetIleGluSerAspLysSerAspLeu.....CysSer 280
837 CTTCTCCAGAGTATCAAGTGAAGTGAACCCGAGCTGCTGCGGCTGCG 886
280 luthrProAsnGlyValLeuGlnValSer 289
887 AGCAGATCGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 915
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seq_name: /cgn2_6/plodata/2/lna/5B_COMB.seq:US-08-460-694-1

seq_documentation_block:

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Sequence 1, Application US/08460694
Patent No. 5858655
GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRAD1 Cyclin and its cDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,694
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McConahly, Evelyn H.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609.4070002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4244 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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232 1aValAlaLeuSerLeuValSerCylgIuLeuGlnAlaValAlHisPheAspAsn 248
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767 GCGTGTGTCGGCCAGTGCAGGCGCTGAACCTGAGG..... 801
249 SerSerPheSerProLeuPheSerLeuLeuGlnIuysGluArValIysIy 265
||||||| ||| ::::
802 .....ACCCCAACAACCTTCTGTCCTACACGCGCTCACACGCTT 842
265 sIeGIyLumetIleGIuSerAspGIySerAspLeu.....CysSerG 280
:::||||:::||||:::||||||
843 CCTCTCCAGAGTGATGCAGTGTGACCCAGACAGTGCCTCGGCGCGCCAGG 892
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893 ACAGATCGAAGCCCTGCTGAGTCAGTCACGC 921

seq_name: /cgn2_6/ptodata/2/lna/5A_COMB.seq:US-08-460-744-1

seq_documentation_block:
Sequence 1, Application US/08460744
Patent No. 6107541
GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF INVENTION: PRADI Cyclin and its cDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,744
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McConathy, Evelyn H.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609,4070005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4244 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 148..1035
US-08-460-744-1

alignment_scores:
Quality: 236.00 Length: 293
Ratio: 1.349 Gaps: 13
Percent Similarity: 59.727 Percent Identity: 28.669

alignment_block:
US-09-530-209A-2 x US-08-460-744-1 ..

Align seg 1/1 to: US-08-460-744-1 from: 1 to: 4244

6 LeuGluLeuSerLeuLeuCysThrGluSerAsnValaIaspGluGlyme 22

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22 ttleValaspGluThrProIleGluIleSerIleProGlnMetClyPheS 39
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39 erGlnSerGluSerGluIleIleMetGluMetValGluIuysGluIys 55
215 TC.....AAGCAACCGGCTCTCGGGCCATGCTGAAGCGGAGAG 255
56 GlnHisLeuProSerAspPylrIleLysArgLeuArgSerGlyAspIe 72
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72 uAspLeuAsnValGlyArgArgAspAlaLeuAsnTrpIleTrpLysAlaC 89
306 GCCGTCCATG.....CGGAAGATCGTCCGACCTGATCTGAGAGTCT 349
89 ysgIuValHisGlnPheGlyProLeuCysPheCysIleAlaMetAsnTyr 105
350 CGGAGGAACAGAGTGCAGAGAGAGGTCTCCCGCTGGCCATGAACTAC 399
106 LeuAspArgPheLeuSerValHisAspLeuProSerGlyLysGlyTrpI 122
400 CTGGACCGCTCTCTGCTGCTGAGCCGTGAAAGAGCGGC..... 441
122 eleuGlnLeuValAlaValaCysLeuSerLeuAlaAlaLysIleGlu 139
442 CTGAGAGTGGTGGGGGCGGCTGATGTTGCTGAGCTTAAAGATGAAG 490
139 lUrThGluValProMetLeuIleAspLeuGlnValGlyAspProGlnPhe 155
491 AGACC...ATCCCGCTG.....ACGGCGGAGAACAGCTGNC 522
156 ValPheGluAlaLysSerValGln.....ArgMetGluLe 167
523 ATCTACACCGCACTCCATCCGCCCGAGAGAGTCTGCAAAATGAGCT 572
167 uLeuValLeuAsnLysLeuLysTrpArgLeuArgAlaIleThrProCys 184
573 GCTCTGGTGGTGAACAGCTCAAGTGAAGTGGCCGCAATGAGCCGAG 622
184 erTyrIleArgTyrPheLeuArgLysMetSerLysCysAspGlnIuPro 200
623 ATTTCATGAAACCTCTCTCCAAATGCA.....GAGCGGAGAGAG 666
201 SerAsnThrIleLeuSerArgSerLeuGlnVal...IleAlaSerThr 216
667 AACAAACAGATCATCCGCAACACGCGCAGACCTTGCTGCTGCTG 716
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717 CACGAGATGAAGTTCATTCCAATCCGCTCCATGATGCGAGCGGGA 766
232 lAvalAlaLeuSerValSerGlyGluLeuGlnArgValHisPheAspAsn 248
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249 SerSerPheSerProLeuPheSerLeuLeuGlnLysGluArgValLys 255
802 .....AGCCCAACCAACTTCTGTCTACTACCGCTCAACACCTT 842
265 sIleGlyLysMetIleGluSerAspGlySerAspLeu.....CysSer 280
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seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-07-667-711B-1

seq_documentation_block:

Sequence 1, Application US/07667711B

Patent No. 6110700

GENERAL INFORMATION:

APPLICANT: ARNOLD, ANDREW

TITLE OF INVENTION: Pradi Cyclin and Its CDNA

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVE., NW, SUITE 600

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/667,711B

FILING DATE: 11-MAR-1991

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MCPHAIL, DONALD R.

REGISTRATION NUMBER: 35,811

REFERENCE/DOCKET NUMBER: 0609,4070000

TELEPHONE: (202) 371-2540

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4244 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: both

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 148..1032

US-07-667-711B-1

alignment_scores:

Quality: 236.00

Ratio: 1.349

Percent Similarity: 59.727

Percent Identity: 28.669

alignment_block:

US-09-530-209a-2 x US-07-667-711B-1

Align seg 1/1 to: US-07-667-711B-1 from: 1 to: 4244

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148 ATGGAAACCACTCTGCTGCTGCGAAGTg..... 177
22 ttleValaspGluThrProIleGluIleSerIleProGlnMetClyPheS 39
178 .....GAAACC...ATCCGCCGCCGTACCCCGATGCCAACCTCC 214
39 erGlnSerGluSerGluIleIleMetGluMetValGluIuysGluIys 55
215 TC.....AAGCAACCGGCTCTCGGGCCATGCTGAAGCGGAGAG 255
56 GlnHisLeuProSerAspPylrIleLysArgLeuArgSerGlyAspIe 72
256 ACCTGGCGCCCTCGGTGCTCTCAATGTGTGCAAGAGAGGTCTCT 305
72 uAspLeuAsnValGlyArgArgAspAlaLeuAsnTrpIleTrpLysAlaC 89
306 GCCGTCCATG.....CGGAAGATCGTCCGACCTGATCTGAGAGTCT 349

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89 ysgluValHisGlnPheGlyProLeuCysPheCysLeuAlaMetAsnTyr 105
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350 GCGAGGAACAAGAGTGGAGAGAGAGTCTTCCCGCTGCGCATGACATAC 399
      ||||| ..... ||||| ..... ||||| ..... |||||
106 LeuAspArgPheLeuSerValHisAspLeuProSerGlyLysGlyTyrP11 122
      ||||| ..... ||||| ..... ||||| ..... |||||
400 CTGGACCGCTCTCTGCTGGAGCCCGTGAAGAAAGAGCCGCGC..... 441
122 eleuGlnLeuLeuAlaValAlaCysLeuSerLeuAlaAlaLysIleGluG 139
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442 CTGCACTCTGTGGGGCCACTGTCATGCTTGGTGGCTCTTAAGATGAGG 490
139 IuThrGluValPrometLeuIleAspLeuGlnValGlyAspProGlnPhe 155
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491 AGACC...ATCCCCCTG.....ACGGCGGAAGAGCTGTGC 522
156 ValPheGluAlaLysSerValGln.....ArgMetGluLe 167
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523 ATCTACACCGCAACTCTCATCCGCCCGAGAGCTGCTGCAATGAGAGCT 572
167 uleuValLeuAsnLysLeuLysTyrParGluArgAlaIleThrProCys 184
      ||||| ..... ||||| ..... ||||| ..... |||||
573 GCTCTGTGGTACAGAGCTCAAGTGAACCTGGCGCATGACCCCGCAGC 622
184 eTyrIleArgTyrPheLeuArgLysMetSerLysCysAspGlnGluPro 200
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201 SerAsnThrLeuIleSerArgSerLeuGlnVal...IleAlaSerThr 216
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667 AACAAACAGATCATCCGCAACACGCGCAGACCTGCTGCTGCTGCTGCTG 716
216 rLysGlyIleAspPheLeuGluPheArgProSer...GlnAlaAlaAla 232
      ||||| ..... ||||| ..... ||||| ..... |||||
717 CACAGATGTAGATTCATTCTCCATCCGCTCATGCTGTCGAGCGGAGG 766
232 IValAlaLeuSerValSerGlyLeuGlnArgValHisPheAsn 248
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767 GCGTGGTGGCGCGAGTCCAGAGCCCTGACCTGAGG..... 801
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265 sIleGlyIleMetIleLeuSerAspGlySerAspLeu.....CysSerG 280
      ||||| ..... ||||| ..... ||||| ..... |||||
843 CCTCTCCAGATGATCAAGTGTGACCCAGACTGCTGCGGCGCTGCCAG 892
280 IuThrProAsnGlyValLeuGluValSer 289
      ||||| ..... ||||| ..... ||||| ..... |||||
893 AGCAGATCGAAGCCCTCTGAGTCAAGC 921

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seq_name: /cgn2_6/plodata/2/lna/5A.COMB.seq:US-08-770-761A-4

seq documentation block:

Sequence 4, Application US/08770761A

Patent No. 5814503

GENERAL INFORMATION:

APPLICANT: Kovacevic, Steven

APPLICANT: Otto, Keith A.

APPLICANT: Rao, Ramachandra N.

TITLE OF INVENTION: FUSION PROTEINS COMPRISING CELL CYCLE

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Eli Lilly and Company

STREET: Lilly Corporate Center/Patent Division

CITY: Indianapolis

STATE: IN

COUNTRY: USA

ZIP: 46285

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,761A
FILING DATE: 19-DEC-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-10136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-376-0756
TELEFAX: 317-277-1917
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4453 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-770-761A-4

alignment_scores:
Quality: 236.00 Length: 293
Ratio: 1.349 Gaps: 13
Percent Similarity: 59.727 Percent Identity: 28.669

alignment_block:
US-09-530-209a-2 x US-08-770-761A-4

Align seq 1/1 to: US-08-770-761A-4 from: 1 to: 4453

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22 tIleValAspGluThrProIleGluIleSerIleProGlnMetGlyPhe 39
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2386 .....GAACCC...ATCCCGCGCGGTACCCGATGCCAAGCTCC 2422
39 erGlnSerGluGlnIleIleMetGluMetValGluLysGluLys 55
      ||||| ..... ||||| ..... ||||| ..... |||||
2423 TC.....AACGACCGGTGCTGCGGCCATGCTAAAGCGGAGAG 2463
56 GlnHisLeuProSerAspPyrIleLysArgLeuArgSerGlyAspLe 72
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2464 ACTGCGCGCGCTGCTGCTGCTTCAATGTCGCAAAAGAGGTCT 2513
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      ||||| ..... ||||| ..... ||||| ..... |||||
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      ||||| ..... ||||| ..... ||||| ..... |||||
2608 CTGACCGCTCTCTGCTGCTGAGCCCGTGAAGAAAGAGCCG..... 2649
122 eleuGlnLeuLeuAlaValAlaCysLeuSerLeuAlaAlaLysIleGluG 139
      ||||| ..... ||||| ..... ||||| ..... |||||
2650 CTGCACTCTGTGGGGCCACTGTCATGCTGTCGCTTAAAGATGAGG 2698
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      ||||| ..... ||||| ..... ||||| ..... |||||
2699 AGACC...ATCCCCCTG.....ACGGCGGAAGAGCTGTGC 2730
156 ValPheGluAlaLysSerValGln.....ArgMetGluLe 167
      ||||| ..... ||||| ..... ||||| ..... |||||
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201 SerAsnThrLeuLeuSerArgSerLeuGlnVal...IleAlaSerThr 216
2875 AACAAACAGATCATCCGCAACACGCGACACCTTCCTGCTTCCTGTGC 2924
216 rLysGlyIleAspPheLeuGlnPheArgProSer...GluAlaIleAla 232
2925 CACAGATGTGAAGTTCATTCCAAATCCGCCCTCCATGTGTGCAGCGGGA 2974
232 IValAlaLeuSerValSerGlyLeuGlnArgValHisPheAspAsn 248
2975 GCGGTGGGCGCGCAGTGCAGGCGCTGAACCTGAGG..... 3009
249 SerSerPheSerProLeuPheSerLeuLeuGlnLysGluArgValLys 265
3010 .....AACCCACACACTTCCTCTCTACTACCGCCTCACACGCTT 3050
265 sileGlyLeuMetIleGluSerAspGlySerAspLeu.....CysSer 280
3051 CCTCTCCAGATGATCAAGTGTGACCCAGACTGCTCCGCGCGCTGCAGG 3100
280 InThrProAsnGlyValLeuGlnValSer 289
3101 AGCAGATCGAAGCCCTGCTGAGTCAACG 3129
seq_name: /cgn2_6/prodata/2/ina/5A_COMB.seq:us-08-770-761A-6
seq_documentation_block:
Sequence 6, Application US/08770761A
Patent No. 5814503
GENERAL INFORMATION:
APPLICANT: Kovacevic, Steven
APPLICANT: Otto, Keith A.
APPLICANT: Rao, Ramachandra N.
TITLE OF INVENTION: FUSION PROTEINS COMPRISING CELL CYCLE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center/Patent Division
CITY: Indianapolis
STATE: IN
COUNTRY: USA
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,761A
FILING DATE: 19-DEC-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-10136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-376-0756
TELEFAX: 317-277-1917
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4540 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-770-761A-6

alignment_scores:
Quality: 236.00 Length: 293
Ratio: 1.349 Gaps: 13
Percent Similarity: 59.727 Percent Identity: 28.669

alignment_block:
US-09-530-209a-2 x US-08-770-761A-6 ..
Align seg 1/1 to: US-08-770-761A-6 from: 1 to: 4540

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22 tLeuValAspGluThrProIleGluIleSerIleProGlnMetGlyPhe 39
2386 .....GAAACG...ATCCGCGCGCGTACCCGATGCCAACCTCC 2422
39 eArgLysSerGluSerGluGluIleIleMetGluMetValGluLysGly 55
2423 TC.....AACGACCGGTGCTCGGCGCATGCTAAAGCGGAGAG 2463
56 GlnHisLeuProSerAspArgTrpIleLysArgLeuArgSerGlyAsp 72
2464 ACCTGCGCGCGCTCGGTGCTCTACTTCATATGTGTCAAAAGAGGTCT 2513
72 uAspLysAsnValGlyArgArgAspAlaLeuAsnTrpIleTrpLysAla 89
2514 GCGGTCCATG.....CGAAGATCGTCCACCTGACCTGATGCTGAGTCT 2557
89 ysgLValHisGlnPheGlyProLeuGlyPheGlyLeuAlaMetAsnTrp 105
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122 eLeuGlnLeuLeuAlaValAlaCysLeuSerLeuAlaIleGln 139
2650 .CTGCACCTCTGCGGCGCCACTGTCATGTTCGCTCTAAAGATGAAG 2698
139 InThrGluValProMetLeuIleAspLeuGlnValGlyAspProGlnPhe 155
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156 ValPheGluAlaLysSerValGln.....ArgMetGluLe 167
2731 ATTCAACACGACATCCATCCCGCCGAGAGCTGCTGCAAAATGAGCT 2780
167 uLeuValLeuAsnLysLeuLysTrpArgLeuArgAlaIleThrProCys 184
2781 GCTCTGTTGAACAAGCTCAAGTGAACCTGCGCCGATGACCCCGACG 2830
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265 sllleGlyMetIleGluSerAspGlySerAspLeu.....CysSerG 280
3051 CCTCTCCAGAGTATCATCAGTCTGACCCAGACGTCGCTCGGCGCTCCAG 3100
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seq_name: /cgn2.6/plodata/2/lna/5B_COMB.seq:US-08-246-361A-3

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seq_documentation_block:
: Sequence 3, Application US/08246361A
: Patent No. 5988582
: GENERAL INFORMATION:
: APPLICANT: BEACH, David H.
: TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
: NUMBER OF SEQUENCES: 50
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LAHIVE & COCKFIELD
: STREET: 60 State Street
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII(text)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/246,361A
: FILING DATE: 19-MAY-1994
: CLASSIFICATION: 435
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 07/963,308
: FILING DATE: 16-OCT-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/888,178
: FILING DATE: 26-MAY-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/701,514
: FILING DATE: 16-MAY-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Matthew P. Vincent
: REGISTRATION NUMBER: 36,709
: REFERENCE/DOCKET NUMBER: MIT-004C
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 227-7400
: TELEFAX: (617) 227-5941
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1911 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 22..888
: US-08-246-361A-3

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alignment_scores:
  Quality: 235.50      Length: 295
  Ratio: 1.323        Gaps: 14
  Percent Similarity: 60.339  Percent Identity: 29.153

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alignment_block:
US-09-530-209A-2 x US-08-246-361A-3
Align seg 1/1 to: US-08-246-361A-3 from: 1 to: 1911

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66 GCGGAGACCGCAACCTGCTCCGAGAC..... 90
34 roGlnMetGlyPheSerGlnSerGlnSerGluGluIleIleMetGluMet 50
91 .....GACCGCTGCTGCAAGACCTG 111
51 ValGluLysGluLysGlnHisLeuProSerAspPylIleLysArgLe 67
112 CTCACCATCGAGAGCGCTACCTTCCGACGTGCTCTACTTCAAGTCCGT 161
67 uArgSerGlyAspLeuAspLeuAsnValGlyArgArgAspAlaLeuAsnT 84
162 GCAGAAAG...GACATCCACCCCTACATG...CGCAGAATGTGGCCACCT 205
84 rPleIleThrPylAspAlaCysGluValHisGlnPheGlyProLeuGlyPheCys 100
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101 LeuAlaMetAsnTyrLeuAspArgPheLeuSerValHisAspLeuProSe 117
256 CTGCCCATGCAATTACTGACCGCTTCTTGGCT.....GGGCTCCGAC 299
117 rGlyLysGlyTyrPleLeuGlnLeuLeuAlaValAlaCysLeuSerLeuA 134
300 TCCGAAGTCCCAT...CTGCAACTCTGGGTGCTGCTGTCATGCTTCCGTG 346
134 lAlaLysIleGluGluThrGluValProMetLeuIleAspLeuGlnVal 150
347 CCTCCAAACTCAAGAGACGAGC...CCGCTG.....ACC 378
151 GlyAspProGlnPheValPheGluAlaLysSerValAlaMetGluLe 167
379 GCGGAGAAAGCTGTGCATTTACCGGACACACTCCATCAAGCTCAGGAGCT 428
167 uLeu.....ValLeuAsnLysLeuLysTyrArgLeuArg 179
429 GCTGAGAGTGGAACTGTGTGCTGGGGAAGTGAAGTGAAGTGAAGTGAAG 478
179 lAlaIleThrProCysSerTyrIleArgIleArgPheLeuArgLysMetSerLys 195
479 CTGTCACTCCTCATGACTTATGAGCAACATCTTGCCAGCTGCCCGCAG 528
196 CysAspGlnGluProSerAsnThrLeuIleSerArgSerLeuGlnVal.. 211
529 .....CAGCGGAGAGAGCTGTCTGTATCCGCAAGCATGCTGACACTT 572
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573 CATGCTCTGTGTGTCACCGCACTTTAAGTTTGGCCATTCACCCAGCGTGA 622
228 Lu...AlaAlaIleAlaValAlaLeuSerValSerGlyGluLeuGlnArg 243
623 TGATGCAACTGGAAGTGTGGAGACACCATCTGTGGCTCCACACGAGAT 672
244 ValHisPheAspAsnSerSerPheSerProLeuPheSerLeuLeuGlnLys 260
673 GAGGAAGTGAAGCTCGTCACACTTGTGATGCCCTGACTGAGCTGGGCTAA 722
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723 GATCACCACACAGACGTGATGTCTCAAAAGCTTTCGAGAGCAGATTTG 772

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177 GCATTGGAGAGCTGAGTTTGTGTCATATAATTAACCTGATAGTT 226
109 eLeuSerValHisAspLeuProSerGlyLeuGlyTrpLeuGlnLeu 126
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227 TCTGTCTTGTATGAAATGCAAGAGTAAATTTGGACAAATTCATTTGT 276
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277 TACCTAGACCTGTTATCCCTGCTGCTCAAAATGGAACAATTAATGTT 326
143 ProMetLeuIleAspLeuGlnValGlyAspProGlnPheValPheGluAl 159
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
327 CCTTGACCTGTTGATTACAGTAGAGGACCTAACTTTTATTGAAAG 376
159 alyssSerValGlnArgMetCysLeuLeuValLeuLysIleLeuLysTrp 175
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
377 CAAACAAATCAAAAGAAATGGAACCTTTGGTGTGAGCACATGACATG 426
176 ArgLeuArgAlaIleThrProCysSerTyrIleArgTyrPheLeuArgI 192
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
427 AGAATGACAGCTTATACACCTTGACATTCATTGATTATTTATGAA 476
192 smetSerLysCysAspGlnGluProSerAsnThrLeuIleSerArgSerL 209
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
477 GATGAAT...CTTGATGAATTCCTCATCGATGCGATTTGTTCTAGATCGA 523
209 euGlnValIleAlaSerThrThrLysGlyIleAspPheLeuGluPheArg 225
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
524 TTCAGCTAAATTAAGCATTAATCAAAAGCTATTGCACTTCTTGAAATTCAGG 573
226 ProSerGluAlaAlaAlaValAlaValAlaLeuSerValSerGlyLeuG 242
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
574 TCTTCTGAATTCAGACAGCAGCAACATCACTG... 609
242 nArgValHisPheAspAsnSerSerPheSerProLeuPheSerLeuG 259
609 ..... 609
259 InLysGluArgValLysLysIleGlyGluMetIleGluSerAspGlySer 275
609 ..... 609
276 AspleuCysSerGlnThrProAsnGlyValLeuGluValSerAlaCysC 292
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
610 .....CCTCAAACTCCAATGGGGGTGTGGAA.....GCTGCTTG 644
292 sPheSerPheLysThrHisAspSerSer 301
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
645 TTGACTACAAAGCTGCGAAGAACAGT 672

seq_name: gb_est1:AM507921
seq_documentation_block: 631 bp mRNA EST 18-JUL-2000
LOCUS AM507921
DEFINITION s147406.y1.Gm-r1030 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-r1030-2027 5' similar to TR:P93103 P93103 CYCLIN-D LIKE PROTEIN.
; mRNA sequence.
ACCESSION AM507921
VERSION AM507921.1 GI:7145999
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 631)
REFERENCE
AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna
,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wylie,T., Underwood,K., Scepioe,M., Theisand,B., Allen,M., Bowers
,V., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
,R., Waterston,R. and Wilson,R.

```

```

TITLE Public Soybean EST Project
JOURNAL Unpublished (1999)
COMMENT Contact: Shoemaker R/Public Soybean EST Project
Public Soybean Est Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
Insert Length: 1012 Std Error: 0.00
High quality sequence stop: 445.
FEATURES
source
1..631
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-r1030-2027"
/clone_id="Gm-r1030"
/lab_host="DH10B"
/note="Vector: pSPORT1, site-1: SalI, Site-2: NotI; This
cDNA library was constructed from mRNA isolated from
immature cotyledons of greenhouse grown plants
(individual seed fresh weight of 100-300mg). The library
was prepared using the Life Technologies Superscript cDNA
library construction kit. Complementary DNA was
synthesized from mRNA using a poly(OT) sequence with a
NotI restriction site. SalI linkers adapted by NotI
to the blunt-ended cDNA fragments were directionally cloned
into the NotI-SalI restriction site of the pSPORT1
vector. The cDNA fragments were of the pSPORT1
into the NotI-SalI restriction site of the pSPORT1
vector. The ligated cDNA fragments were transformed into
E. coli Electromax DH10B host cells. This library was
constructed by Dr. Lila Vodkin and Dr. Ann Khanna. Note
that Gm-r1030 is a re-track of Gm-c1007."
BASE COUNT 184 a 117 c 145 g 185 t
ORIGIN
alignment_scores:
Quality: 495.00 Length: 192
Ratio: 3.278 Gaps: 4
Percent Similarity: 78.646 Percent Identity: 53.125
alignment_block:
us-09-530-209a-2 x AM507921 ..
Align seg 1/1 to: AM507921 from: 1 to: 631
101 LeuAlaMetAsnTyrLeuAspArgPheLeuSerValHisAspLeuProSe 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
8 CTACTATAATTAATCTTGAGCCGATTCCTCTTGCAATATCAATACCGAA 57
117 rGlyLysGlyTrpIleLeuGlnLeuAlaValAlaCysLeuSerLeuAl 134
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
58 GCGAAGAGTTGGACAAATGCAATGTGCGCTGCGCTGTTATCTCTAG 107
134 AlaAlaLysIleGluGluThrGluValProMetLeuIleAspLeuGlnVal 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
108 CAGCCAAATTAAGATGACAGCAAGTTCACCTCTCTTGATTTGCAGTG 157
151 GlyAspProGlnPheValPheGluAlaLysSerValGlnArgMetCysLe 167
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
158 GGTGAATCGAAGTTTATTGAGGCTAAACCATACAGAAATGAGAGCT 207
167 uLeuValLeuAsnLysLeuLysTrpArgLeuArgAlaIleThrProCys 184
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
208 TCTTGACTAGACACATTAAGATGAGAAATCAAGCAATTAATCTCTTCA 257
184 eTyrIleArgTyrPheLeuArgLysMetSerLysCysAspGlnGluPro 200

```

```

258 CTTTCCTGATTAATCTTTGTAAGTCAACGAT...GATCAAGTCCA 304
      ::::: ||||| ::::: |||||
201 SerAsnThrLeuIleSerArgSerLeuGlnValIleAlaSerThrIly 217
      ::::: || ||||| ::::: |||||
305 TTAAGCTTCAATTAATGCGATCCATCCAACTATATATCGAGCACTGCAG 354
217 SGVILLeaSPheLeuGlnPheArgProSerGluAlaIleAlaVala 234
      ::||| ::||| ::||| ::||| ::||| ::|||
355 AGGATTGACTTCTTGCAATTTAAACCATCAGAGATTGACGACGACGTGG 404
234 ILeuSerValSerGlyIleLeuGlnArgVal..HisPheAspAsnSer 250
      ::||| ::||| ::||| ::||| ::||| ::|||
405 CTATGATGATGATGCGGGGAAACCAACACTTGACACTGGGAAAGCATG 454
250 erPheSerProLeuPheSerLeuLeuGlnIlySerGluArgValLysIly 266
      ::||| ::||| ::||| ::||| ::||| ::|||
455 TCTGTTCT.....GATTCACACGCTAGATA 480
267 GYGLumetIleGlySerAspGlySerAspLeuGlySerGlnThrProAs 283
      ||||| ||||| ::||| ::||| ::||| ::|||
481 GGAGAGACTTTGAA.....GTGTTTCAATGATCCGAG 515
283 nGlyValLeuGlnValSerAlaCys 291
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516 AGGTATCATGCAACAGTGCCTGC 540

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seq_name: gb_ect1:BE442681

seq_documentation_block:

LOCUS BE442681 621 bp mRNA EST 25-JUL-2000
DEFINITION WHE1101_A09_A17Zs wheat etiolated seedling root normalized cDNA
library Triticum aestivum cDNA clone WHE1101_A09_A17, mRNA
sequence.

ACCESSION BE442681 GI:9442114

VERSION BE442681

KEYWORDS EST.

SOURCE bread wheat.

ORGANISM Triticum aestivum

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Triticum.
1 (bases 1 to 621)

AUTHORS Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.

TITLE The structure and function of the expressed portion of the wheat
genomes - Normalized root cDNA library
Unpublished (2000)

JOURNAL Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818

COMMENT Email: oanderson@w.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stralagene SK primer.
Location/Qualifiers

FEATURES
1..621
source

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/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1101_A09_A17"
/clone_lib="Wheat etiolated seedling root normalized cDNA
library"
/tissue_type="Root"
/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
/note="Vector: lambda uni-zap XR, excised phagemid
pluscript SK; Site 1: EcoRI; Site 2: XhoI; Seeds were
surface-sterilized, germinated and grown aseptically in

```

the dark at room temperature on filter paper with water,
nystatin and cefotaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared, a cDNA library was made in the
TJ Close lab (Choi, Close, Fenton) at the University of
California, Riverside. The cDNA clones were in vivo
excised to give pluscript phagemids before
normalization was carried out. The mass excision of
phagemid library and normalization were done in HT Nguyen
lab by D. Zhang at Texas Tech University. Normalization
protocol used was that of Soares. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors).

BASE COUNT 142 a 157 c 156 g 166 t
ORIGIN

alignment_scores:
Quality: 468.00 Length: 209
Ratio: 3.059 Gaps: 4
Percent Similarity: 73.206 Percent Identity: 50.239

alignment_block:
US-09-530-209a-2 x BE442681 ..

Align seg 1/1 to: BE442681 from: 1 to: 621

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1  CCCTTGACCTCGCGCTGCTGCTCAACACTGATAGTTCCTCCCTCCG 50
112 IHisAspLeuProSerGlyIlySerGlyTyrPheLeuGlnLeuAlaVala 129
      ::||| ::||| ::||| ::||| ::||| ::|||
51 CTATCCCTTCGTAAGCAAGCAACCTGGGACACACCTCTGGCACTGG 100
129 IAcysLeuSerLeuAlaAlaLysIleGlnIleThrGlnValPrometLeu 145
      ||||| ::||| ::||| ::||| ::||| ::|||
101 CTTCCTGCTCCCTCCCTGCTCAACATGAGAGAGACTATGTCCTCC 150
146 ILeaSPheLeuGlnValGlyAspProGlnPheValPheGlnAlaLysSerVa 162
      ::||| ::||| ::||| ::||| ::||| ::|||
151 GTCACCTCGCAGGTTGTTGAGGCAAAATTCGCTTCAGGGAAGACCAT 200
162 IGlutArgMetGlnLeuValLeuAlaLysIleValLysTyrArgLeuArg 179
      ::||| ::||| ::||| ::||| ::||| ::|||
201 AAAAAGATGAGAGCTTGTGCTCACACCTTAATAATGAGAGTGCAG 250
179 IAlaThrProCysSerTyrIleArgTyrPheLeuArgLysMetSerLys 195
      ::||| ::||| ::||| ::||| ::||| ::|||
251 CTGTTACTGCTGCTCATTTATTCACACTTCCTCCGCCAATTCATGAT 300
196 CysAspGlnIleProSerAsnThrLeuIleSerArgSerLeuGlnVal 212
      ::||| ::||| ::||| ::||| ::||| ::|||
301 CATGAC...GGCCCTCCATGCTGCTGCTCCGCTCGACCGACCTCAT 347
212 eAlaSerThrThrLysGlyIleAspPheLeuGlnPheArgProSerLys 229
      ::||| ::||| ::||| ::||| ::||| ::|||
348 CCTGACGACAGCTTAAGAGACTGATTTTGTGCTTCAGACCTTCAGAGA 397
229 IAlaAlaAlaValAlaLeuSerValSerGlyIleGlnArgValHis 245
      ::||| ::||| ::||| ::||| ::||| ::|||
398 TTGCTGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 447
246 PheAspAsnSerSerPheSerProLeuPheSerLeuLeuGlnIlyGlu 262
      ::||| ::||| ::||| ::||| ::||| ::|||
448 GTCAGAGCGGCTACACTACTTGCACATTC.....ATAAACAAGAGCG 491
262 gValLysLysIleGlyLumetIleGlu..... 271
      ::||| ::||| ::||| ::||| ::||| ::|||
492 AGTGTTAAGATGCTACGATTAATTAAGCAAGCAATGACATGGAACCA 541
272 .....SerAspGlySerAspLeuGlySer.....GlnThrPro 282
      ||| ||||| ::||| ::||| ::||| ::|||

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542 TTGCTTAAAGTCAGCTGCATCATCATGTTCTGTGCGCAAGCCCG 591
283 AsnGlyValLeuGluValSerAlaCys 291
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592 ATATGCTGTGGATGCTGCTGCATGT 618
seq_name: gb_est2:B1306295

seq_documentation_block:
LOCUS B1306295 790 bp mRNA EST 20-JUL-2001
DEFINITION NL_4_B12 Drought stress (leaf) Oryza sativa cDNA clone NL_4_B12 3',
mRNA sequence.
ACCESSION B1306295
VERSION B1306295.1 GI:14981617
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 790)
Reddy,A.R., Ramakrishna,M., Chandrasekhar,A., Nagabhusan,I.,
Ravindrababu,P. and Bennetzen,J.L.
Novel EST enrichment with normalized cDNA libraries from drought
stressed rice (Oryza sativa L.cv Nagina 22)
Unpublished (2001)
JOURNAL Contact: Reddy AR
Department of Plant Sciences, School of Life Sciences
University of Hyderabad
P.O. Central University, Hyderabad-500 046, A.P, India
Tel: 0091-40-3010265
Fax: 0091-40-3010145
Email: arjuls@uohyd.ernet.in
Insert Length: 790 Std Error: 0.00
Plate: 4 row: B column: 12
Seq primer: GTAAACGACGCGCCAGTG.
FEATURES
source 1..790
/organism="Oryza sativa"
/cultivar="Nagina 22 (indica sub sp)"
/db_xref="taxon:4530"
/clone="NL_4_B12"
/clone_lib="Brought stress (leaf)"
/tissue_type="Entire leaf tissue"
/dev_stage="35 day-old seedlings"
/note="Organ: Leaf; Vector: pT73pac; ESTs from normalized
leaf cDNA library from drought stressed seedlings"
BASE COUNT 222 a 239 c 179 g 150 t
ORIGIN
alignment_scores:
Quality: 443.00 Length: 185
Ratio: 3.120 Gaps: 2
Percent Similarity: 76.757 Percent Identity: 48.649
alignment_block:
US-09-530-209a-2 x B1306295/rev ..
Align seg 1/1 to reverse of: B1306295 from: 1 to: 790
42 GUGserGluGluIleIleMeGluMeValGluGlyGlnHisLe 58
|||||:|||||:|||||:|||||:
596 GACGTCCGATGAGTTCGTGCGCTGTTGTTGTCGAGAGGAGGATGATCATCA 547
58 uprSeraspAspTyrIleLysArgLeuArgSerGlyAspLeuAspLeuA 75
|||||:|||||:|||||:|||||:
546 GCCCTACGCGGGGATATCTGGAAGAGCTGAGAGCTGCGATTTGAGGTGT 497
75 snValGlyArgArgAspAlaLeuAsnTPrIleTPrLysAlaCysGluVal 91
|||||:|||||:|||||:|||||:
496 CT...TGAGAGAAAGATGCCATTTGATTGATTCGCAAGTCCATTCCTAC 450

```

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92 HisGlnPheGlyProLeuGlySphGlySLeuAlaMetAsnTyrLeuAsp 108
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449 TACAACTTTGACCACTGACCCCTTACCTCGCATGAGTAACTACTGATG 400
108 gPheLeuSerValHisAspLeuProSerGlyLysGlyTPrIleLeuGln 125
|||||:|||||:|||||:|||||:
399 GTTCCTCTCTCCTGTTAATCTCCCTCATGACGAATCTTGATGCACACGT 350
125 euLeuAlaValAlaCysLeuSerLeuAlaAlaLysIleGluGlu 141
|||||:|||||:|||||:|||||:
349 TGCTGTCATGACTAGTCTATCTCTGCTACGAAGATGAGAGACCGTG 300
142 ValProMetLeuIleAspLeuGluValGlyAspProGlnPheValPheG 158
|||||:|||||:|||||:|||||:
299 GTCCCTCTTCCCATGAGACCTTCAGGTTTGTGATGCGGAATATGTGTGA 250
158 uAlaLysSerValGlnArgMetGluLeuValLeuAsnLysLeuLysT 175
|||||:|||||:|||||:|||||:
249 AGCAGGCATATTAGAGATGAGATGAGCTTATTGTATGAAACCCCTGAAT 200
175 rPArgLeuArgAlaIleThrProCysSerTyrIleArgTyrPheLeuArg 191
|||||:|||||:|||||:|||||:
199 GGAGGCTGCAGAGCTGTGACCCCATCTCTTTCATTCGCGTACTCTTGAC 150
192 LysMetSerLysCysAspGlnGluProSerAsnThrLeuIleSerArgSe 208
|||||:|||||:|||||:|||||:
149 AAGTTCAATCAA...GGAGACCCGCGAGCTACACGCTGCATCATGCTG 103
208 rLeuGlnValIleAlaSerThrThrLysGlyIleAspPheLeuGluPheA 225
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102 CTCGTATCTCAGATGAGCGACCTCTGAAGAGCTAGTCTGTCTCATTTCA 53
225 rGPro 226
|||||
52 GACCT 48
seq_name: gb_est2:BG585146

seq_documentation_block:
LOCUS BG585146 809 bp mRNA EST 11-APR-2001
DEFINITION EST186909 MHAM Medicago truncatula/Glomus versiforme mixed EST
library cDNA clone PMHAM-22A23 5' end, mRNA sequence.
ACCESSION BG585146
VERSION BG585146.1 GI:13600210
KEYWORDS EST.
SOURCE Medicago truncatula/Glomus versiforme mixed EST library.
ORGANISM Medicago truncatula/Glomus versiforme mixed EST library.
Eukaryota; mixed EST libraries.
1 (bases 1 to 809)
REFERENCE Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Uterback,T., Cho,J.
and Fraser,C.M.
Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Uterback,T., Cho,J.
and Fraser,C.M.
TITLE Glomus versiforme, 2001
ESTs from roots of Medicago truncatula after colonization with
JOURNAL Glomus versiforme, 2001
CONTACT: Harrison M.J.
UNPUBLISHED (2001)
JOURNAL Plant Biology Division
CONTACT: Harrison M.J.
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401
Tel: 580-223-5810
Fax: 580-221-7380
Email: mjharrison@noble.org
Noble EST name: N380619e TIGR sequence name: WMDCA127K More
information is available at: http://www.medicago.org
Seq primer: SKmod (CTA gAA CTA gTg gAT CC).
FEATURES
source 1..809
/organism="Medicago truncatula/Glomus versiforme mixed EST
library"
/cultivar="Medicago truncatula genotype A17"
/db_xref="taxon:119092"
/clone="PMHAM-22A23"
/clone_lib="MHAM"
/tissue_type="roots colonized with Glomus versiforme"

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/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The library was made from a mixture of RNA from each of these stages."
 /lab_host="E. coli strain XL0LR"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA from roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The cDNA was directionally ligated into the UniZap XR vector from StrataGene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-zap phage using Ex-assist helper phage and propagated in XL0LR cells."

BASE COUNT 194 a 196 c 173 g 246 t
 ORIGIN

alignment_scores:

Quality: 428.00 Length: 256
 Ratio: 2.474 Caps: 6
 Percent Similarity: 67.578 Percent Identity: 38.672

alignment_block:

US-09-530-209a-2 x BG585146 ..

Align seg 1/1 to: BG585146 from: 1 to: 809

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7  GluLeuSerLeuLeuGlyThrGluSerAsnValAspAspGluGlyMetI 23
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31  GACTGCGACCTCTCTCGCGGAG.....GACTCGTCGAGCTCTCT 71
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
23  evalAspGluThrProLeuGluLeuSer.....GCTGCTCTCTCT 32
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
72  CACCGGAGTTTACCG..GAATGCTCTCTCCGACCTGATTCATTCAT 118
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
33  .....IleProGluMetGlyPheSerGlnSerGluSerGluGlu 46
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
119  CATCGCAGTTGCGCGTCGTCATTTATTCGCGAGAGAGAGAGAGAGTCG 168
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
47  IleMetGluMetValGluGlyGlnHisLeuProSerAspSply 63
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
169  ATTGCTGTTTTCATCGACGACGATTGCTGCTGCTGCTGCTGCTGCT 218
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
63  rIleLysArgLeuArgSerGlyAspLeuAspLeuAsnValGlyArgArg 80
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
219  CGTCTCAAGATTTCATTCGCTCTCTCGAATCCACACACC..AGAGAA 265
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
80  spAlaLeuAsnTrpIleTrpLysAlaCysGluValHisGlnPheGlyPro 96
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
266  AACCCATTGCATGATTCACAGTACATGATATGATATGATTTTCAGCG 315
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
97  LeuGlyPheCysLeuAlaMetAsnTrpLeuAspArgPheLeuSerValH 113
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
316  TTAACGCGCTACCTCTCGTTACTATGATGCGTTTGGATCTCTCT 365
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
113  sAspLeuProSerGlyLysGlyTrpIleLeuGlnLeuAlaValAlaC 130
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
366  ACCTTTACCGGAATCAATGATGCGCACTGCAACTTTTATCTGTGAT 415
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
130  ylsLeuSerLeuAlaAlaLysIleGluGluThrGluValProMetLeu 146
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
416  GTTTCCTTACGACGAAGAATGAGAGAACCACTGCTCTCTCTCTT 465
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
147  AspLeuGlnValGlyAspProGlnPheValPheGluAlaLysSerVal 163
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
466  GATTTTCAGATTGAGCGTCCCAATATATTTCACCAAGAGAGATTC 515
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
163  natGmetGluLeuLeuValLeuAsnLysLeuLysTrpArgLeuArgAla 180
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
516  TAGAATGAGACCTCTCTCTGCTGCTATTTTGGATGGAGGCTGATCAA 565
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
180  leThrProCysSerTrpIleArgTrpPheLeuArgLysMetSerLysCys 196
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|

```

```

566  TCACCCCACTTAGTTTCCTCAGTTTCTT.....CGCTGC 600
197  AspGluGluProSerAsnThr.....LeuIleSerArgSerLe 209
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
601  AACCTAGATTCACTGCACTTTCACCCCACTTCATATTTTCAGCTCTAC 650
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
209  uGlnValIleAlaSerThrThrLysGlyIleAspPheLeuGluPheArg 226
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
651  AGAATCATCTTATCTAATATCCAGATGCTACTTCTTACTTACAGGC 700
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
226  roSerGluAlaAlaAlaValAlaLeuSerValSerGlyGluGln 242
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
701  CATCATGATTCGTCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 750
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
243  ArgValHisPheAspAsn 248
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|
751  AATTGCTCTTTTCTTAT 768
   :::::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|

```

seq_name: gb_est2:BG646052

seq_documentation_block: 810 bp mRNA

LOCUS BG646052 EST 24-APR-2001
 DEFINITION EST507671 KV3 Medicago truncatula cDNA clone PKV3-48G20 5' end,
 mRNA sequence.

ACCESSION BG646052

VERSION BG646052.1 GI:13781164

KEYWORDS EST.

SOURCE

ORGANISM

Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
 Medicago.

REFERENCE 1 (bases 1 to 810)

AUTHORS Vandenbosch,K., Endre,G., Hur,J., Beremand,P., Town,C.D., Bowman
 C.L., Craeven,M.B., Cho,J. and Fraser,C.M.

TITLE ESTs from roots of Medicago truncatula 72 h after Rhizobium
 inoculation, 2001

JOURNAL Unpublished (2001)

CONTACT Vandenbosch K
 Department of Biology
 Texas A&M University

College Station, TX 77843-3258, USA
 Tel: 409 845 7707
 Fax: 409 845 2891

Email: kate@mail.bio.tamu.edu
 M394459e TIGR sequence name: MTECU46TK More information is
 available at: www.medicago.org

Seq primer: SKmod (CTA GAA CTA
 Location/Qualifiers

FEATURES

SOURCE

1..810
 /organism="Medicago truncatula"
 /cultivar="genotype A17"
 /db_xref="taxon:3880"

/clone="PKV3-48G20"
 /clone_lib="KV3"

/tissue_type="Seedling roots"
 /dev_stage="3 days post-inoculation with Sinorhizobium
 meliloti"

/lab_host="E. coli strain XL0LR"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
 XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
 was directionally ligated into the UniZap XR vector from
 StrataGene and packaged using Gigapack III Gold packaging
 extracts. Plasmids containing cDNA inserts were excised
 from the recombinant lambda-zap phage using Ex-assist
 helper phage and propagated in XL0LR cells."

BASE COUNT 195 a 201 c 170 g 244 t

ORIGIN

alignment_scores: Quality: 426.50 Length: 266


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50 tValGluLysGluLysGlnHisLeuProSerAspPtyrIleLysArgL 67
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154 CATGAGACGACGACTTCAAGTTTGTCTGCTTCGACTGATGCTCAAGAT 203
   ::::: ||| ::::: ||| ::::: ||| ::::: |||
67 euArgSerGlyAspLeuAspLeuAsnValGlyArgArgAspAlaLeuAsn 83
   ::::: ||| ::::: ||| ::::: ||| ::::: |||
204 TCCAAATCTGCTCTCGAATCCAGACC...AGAGAAAGACCATTTGCA 250
   ::::: ||| ::::: ||| ::::: ||| ::::: |||
84 TrpIleTrpAlaCysGluValHisGlnPheGlyProLeuGlyPheCys 100
   ||||| ||||| ||||| ||||| ||||| |||||
251 TGGATTCTCAAGGTACATGATGATGATGATGATGATGATGATGATGAT 300
   ||||| ||||| ||||| ||||| ||||| |||||
100 sLeuAlaMetAsnTyrLeuAspArgPheLeuSerValHisAspLeuPro 117
   ||||| ||||| ||||| ||||| ||||| |||||
301 CTTCTCGCTTAATGATGATGATGATGATGATGATGATGATGATGATGAT 350
   ||||| ||||| ||||| ||||| ||||| |||||
117 eArgLysGlyTrpIleLeuGlnLeuLeuAlaValAlaCysLeuSerLeu 133
   ::::: ||||| ||||| ||||| ||||| ||||| |||||
351 AATCAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 400
   ::::: ||||| ||||| ||||| ||||| ||||| |||||
134 AlaAlaLysIleGluGluThrGluValProMetLeuIleAspLeuGln 150
   ||||| ||||| ||||| ||||| ||||| |||||
401 GCAGCAAGATGAGGAGGACCACTGTTCTCTCTCTCTCTCTCTCTCT 450
   ||||| ||||| ||||| ||||| ||||| |||||
150 LgIAspProGlnPheValPheGluAlaLysSerValGlnArgMetGln 167
   ||||| ||||| ||||| ||||| ||||| |||||
451 TGAAGTGCCTCAATATGATGATGATGATGATGATGATGATGATGATGAT 500
   ||||| ||||| ||||| ||||| ||||| |||||
167 euLeuValLeuAsnLysLeuLysTrpArgLeuArgAlaIleThrProCys 183
   ||||| ||||| ||||| ||||| ||||| |||||
501 TGTCTGTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 550
   ||||| ||||| ||||| ||||| ||||| |||||
184 SerTyrIleArgTyrPheLeuArgLysMetSerLysCysAspGlnIupr 200
   ||||| ||||| ||||| ||||| ||||| |||||
551 AGTTTCTCTGATTTCTTT...GCCTGCAAGCTAGATTC 585
   ||||| ||||| ||||| ||||| ||||| |||||
200 oSerAsnThr...LeuIleSerArgSerLeuGlnValIleA 213
   ||||| ||||| ||||| ||||| ||||| |||||
586 AACTGGAACTTCAACCCACTTCAATATTCAGCTGCTACAGAAATCATCT 635
   ||||| ||||| ||||| ||||| ||||| |||||
213 lAserThrThrLysGlyIleAspPheLeuGlnPheArgProSerGluAla 229
   ||||| ||||| ||||| ||||| ||||| |||||
636 TATCTAATATCCAAAGATGCTAGCTTCTTCTTCTACAGGCCATATGAT 685
   ||||| ||||| ||||| ||||| ||||| |||||
230 AlaAlaValAlaLeuSerValSerGlyGluLeuGlnArgValHisPh 246
   ||||| ||||| ||||| ||||| ||||| |||||
686 GCTGCAAGTGCCTACTCTCTCTGAGCTAATGAATTCCTAATTTGCTCT 735
   ||||| ||||| ||||| ||||| ||||| |||||
246 eAspAsn 248
   ||||| ||||| ||||| ||||| ||||| |||||
736 TGTTAAT 742
   ||||| ||||| ||||| ||||| ||||| |||||
seq_name: gb_est2:BG585934
seq_documentation_block:
LOCUS BG585934 834 bp mRNA EST 11-APR-2001
DEFINITION E17487699 MHAM Medicago truncatula/Glommus versiforme mixed EST
library cDNA clone PMHAM-31L19 5' end, mRNA sequence.
ACCESSION BG585934
VERSION BG585934.1 GI:13600998
KEYWORDS EST
SOURCE Medicago truncatula/Glommus versiforme mixed EST library.
ORGANISM Medicago truncatula/Glommus versiforme mixed EST library.
REFERENCE 1 (bases 1 to 834)
AUTHORS Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Utterback,T., Cho,J.
and Fraser,C.M.
TITLE ESTs from roots of Medicago truncatula after colonization with
Glommus versiforme, 2001
JOURNAL Unpublished (2001)
COMMENT Plant Biology Division

```

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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401
Tel: 580-223-5810
Fax: 580-221-7380
Email: mjharrison@noble.org
Noble EST name: N381409e TIGR sequence name: MTDCk707K More
information is available at: http://www.medicago.org
Seq primer: SKmod (CTA GAA CTA gta gAT CC).
FEATURES
source
1. 834
/organism="Medicago truncatula/Glommus versiforme mixed EST
library"
/cultivar="Medicago truncatula genotype A17"
/db_xref="taxon:119092"
/clone="PMHAM-31L19"
/clone_lib="MHAM"
/lisue_type="Roots colonized with Glommus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glommus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host="E. coli strain XLOLR"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glommus versiforme. The cDNA was
directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
BASE COUNT 198 a 205 c 176 g 255 t
ORIGIN
alignment_scores:
Quality: 422.50 Length: 266
Ratio: 2.414 Gaps: 7
Percent Similarity: 65.789 Percent Identity: 37.594
alignment_block:
US-09-530-209A-2 x BG585934 ..
Align seg 1/1 to: BG585934 from: 1 to: 834
1 MetAlaGluLysAsnLeu..... 6
||| ||||| ::::: |||
32 ATGATTGAAAGCAATTCATGCGCAATTCATGCGCACTGTCACACCTC 81
||| ||||| ::::: |||
7 GluLeuSerLeuGluCysThrGluSerAsnValAspAspGluGlyMetI 23
::: ||||| ||||| |||
82 CGACTGCGAGCTCTCTGCGGGAG.....GACTCTGTGGAGGTCC 122
||| ||||| ||||| |||
23 LeuAlaSpGluThrProIleGluIleSer..... 32
::::: ::::: ||| |||
123 TCAACCGAGATTTACCG...GAATGCTCTCCGACCTCGATTCATCATCA 169
||| ||||| ::::: |||
33 .....IleProGlnMetGlyPheSerGlnSerGluSerGluIuI 46
::::: ||||| ::::: |||
170 TCATTCGCGAGTTGCCCTGCTCATTTATTCGCCGAGCAAGGAGGAGTC 219
||| ||||| ||||| |||
46 eIleMetGluMetValGluLysGluLysGlnHisLeuProSerAspSPT 63
::::: ||||| ||||| |||
220 GATTGCTGTTTTCATCGACGACGAGTTCAAGTTGTTCTGCTTTCACACT 269
||| ||||| ||||| |||
63 TyrIleLysArgLeuArgSerGlyAspLeuAsnValGlyArgArg 79
::::: ||||| ::::: |||
270 ACGTCTCAAGATTCATTCGCTCTCGAATCCAGCACC...AGAGAA 316
||| ||||| ||||| |||
80 AspAlaLeuAsnTrpIleTrpLysAlaCysGluValHisGlnPheGlyPr 96
::::: ||||| ||||| |||
317 GAAGCCATTCATGATGATTCCAAGGTACATGATGATGATGATGATGATGAT 366
||| ||||| ||||| |||
96 oLeuGlyPheCysLeuAlaMetAsnTyrLeuAspArgPheLeuSerValH 113

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|||||
367 GTTAACGGCGTACCTCCGTTAACTATATGATCGGTTTTCGATTC 416
113 isaspleuproserglylysrpilleuglnleuvala129
417 GACCTTACCGGAATCAATGATGGCAGCTGCACTTTATCTGTTGCA 466
130 CysleuSerleuA1a1a1ysIleGluGluValPromeIeu1 146
467 TCTTGTCTTACGACCAAGATGAGAGACCACTGTTCTCTCTCT 516
146 eaapleuGlnValGlyasproGlnPheValPheGluAlaLysSerValG 163
517 AGACTTTCAGATTGAAGTGCACCAATACATATTTCAACAGAGCGATT 566
163 InArgmetGluLeuValLeuAsnLysLeuLysTrpArgLeuArgAla 179
567 TTGGAATGAGCTGCTTCTTCTGACTATTTGGATTGGAGCTGAGATCA 616
180 IleThrProCysSerTyrlleArgTyrPheLeuArgLysMetSerLysCy 196
617 ATCACCCTAGTAGTTCTCAGCTTCTT.....GCGTG 651
196 sasplnglnIProSerAsnThr.....LeuIleSerArgSerL 209
652 CAAGCTGATGCACTGGAAGTTCACCCACTTCATATTTTTCAGCTGCTA 701
209 euglnValIleAlaSerThrThrLysGlyIleAspPheLeuGluPheArg 225
702 CAGAAATCATCTATCTAATATCCAGATGCTGCTTCTTACTTAAGG 751
226 ProSerGlnA1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1a1 241
752 CCATCATGATCTGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 799

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seq_name: gp_est1:BE642779

seq_documentation_block:

LOCUS BE642779 813 bp mRNA EST 01-SEP-2000
 DEFINITION Cr12_6_P20.SP6 Ceratopteris Spore Library Ceratopteris richardii
 CDNA clone Cr12_6_P20 5', mRNA sequence.

ACCESSION BE642779
 VERSION BE642779.1 GI:9960458

KEYWORDS EST.

SOURCE

ORGANISM Ceratopteris richardii.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Filicophyta; Filicopsida; Filicales; Pteridaceae; Ceratopteris.

REFERENCE 1 (bases 1 to 813)
 Chatterjee,A., San Miguel,P., Stout,S.C., Banks,J. and Roux,S.J.
 Expressed sequence tags of cDNA clones from a C. richardii library

JOURNAL Unpublished (2000)

COMMENT Section of Molecular Cell and Developmental Biology
 University of Texas
 Biology Building, Room 16, Austin, TX 78712, USA

Tel: 512 471 4238
 Fax: 512 232 3402
 Email: sroux@uts.cc.utexas.edu

Plate: Cr12_6 row: P column: 20

Seq primer: SP6.

FEATURES

source Location/Qualifiers

1..813
 /organism="Ceratopteris richardii"
 /cultivar="Brogan"
 /db_xref="taxon:49495"
 /clone="Cr12_6_P20"
 /clone_lib="Ceratopteris Spore Library"
 /tissue_type="gametophyte"
 /cell_type="Spore"
 /dev_stage="20 hours after germination initiation"
 /note="Vector: PCWSPORTE; EST sequence from cDNA library.
 cDNA library constructed from mRNA isolated from C."

richardii spores that had developed for 20 hours after
 their germination had been initiated by white light."

BASE COUNT 196 a 169 c 191 g 257 t
 ORIGIN

alignment_scores:

Quality: 401.50 Length: 241
 Ratio: 2.419 Gaps: 5
 Percent Similarity: 68.880 Percent Identity: 40.249

alignment_block:

US-09-530-209a-2 x BE642779

Align seg 1/1 to: BE642779 from: 1 to: 813

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78 ArgArgspAlaLeuAsnTrpIleTrpLysAlaCysGluValHisGlnP 94
|||||
10 CGGACAGAGGCGCATTCAGCTGATTTCTAAGCTTCGAGATTCTACAA 59
94 eGlyProLeuCysPheCysLeuAlaMetAsnTyrLeuAspArgPheLeu 111
|||||
60 TGGCGCTTTGACTGTGCGCTCTGTGAACTACGTTGATGATTCCTT 109
111 erValHisAspleuproserglylysrpilleuglnleuvala127
|||
110 CTTGTCAAAGATCCGCGTGAAGAACCGTGATGATGATGATGATGATG 159
128 ValAlaCysLeuSerleuA1a1a1a1a1a1a1a1a1a1a1a1a1a1a 144
|||||
160 GTGCGATGATTCATTCATTCGCTGCAAAATGCAAGATGAGAGTCCGT 209
144 tLeuIleAspleuGlnValGlyasproGlnPheValPheGluAlaLys 161
|||||
210 ATTGCTGACCTTCACGCT...GATCCAGAGTGTCTTGAACCTCGCA 256
161 erValGlnArgMetGluLeuValLeuAsnLysLeuLysTrpArgLeu 177
|||||
257 CAATTCACGATGAGACTGCTGCTGAGCACTTTCGATGAGCAATG 306
178 ArgAlaIleThrProCysSerTyrlleArgTyrPheLeuArgLysMet 194
|||||
307 AGTCTGCTGACACCATTTGCTATATAGACTGCTGATGATCAATGTA 356
194 rLysCysAspGlnIuProSerAsnThrLeuIleSerArgSerLeuGln 211
|||||
357 C...CTCGATTGACAGCTTCATTCCTCTCTCCGCTGCTGCTGAGC 403
211 alIleAlaSerThrThrLysGlyIleAspPheLeuGluPheArgPro 227
|||||
404 TTATTTTGTGCGCTATTCAGAGAGCTTAATTTCTCTTCCGGCCATCT 453
228 GlnAlaAlaAlaAlaAlaLeuSerValSerGlyLys.....Le 241
|||||
454 GCCATTCGCTGTCATCCATTCGTGTGTCAGTGCAGAGCTGATTCAT 503
241 uGlnArgValHisPheAspAsnSerSerPheSerProLeu..... 254
|||||
504 GGAACCTTACTAACTTAAGGAGCTTATCTCTGTATGATCCGGCACAG 553
255 .....PheSerLeuGlnLysGluArgVal 263
|||||
554 TGCAGATACATGTAAGATGCTTTACCTGCTGCTGCTGCTGCTGCT 603
264 LysLysIleGlyLysMetIleGluSerAspLysSerAspLysCysSer 279
|||||
604 TTGACACCATTTACATGATGTCAGATGAAATATATTTTGTGACAC 653
280 GlnThrProAsnGlyValLeuGlnValSerAlaCysCysPheSerPhe 296
|||||
654 TAGACGCGCTATCGAGTGTGATGCTTCAATTTAGTTGACAGTGA 703
296 ysrThrHisAspSerSerSer 303

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704 GCACATTGAAGTCAGCGGCTCT 726

seq_name: gb_est2:BG726093

seq_documentation_block:

LOCUS BG726093 498 bp mRNA EST 09-MAY-2001
DEFINITION sae06b09.y1 Gm-cl055 glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-cl055-4578 5' similar to TR:Q9ZRX9 Q9ZRX9 CYCLIN D2.1
PROTEIN: mRNA sequence.

ACCESSION BG726093 GI:14011162

VERSION EST

KEYWORDS

SOURCE

ORGANISM

Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 498)

REFERENCE

AUTHORS

Shoemaker, R., Keim, P., Vodka, L., Erpelid, J., Corryell, V., Khanna,
'A', Bolla, B., Maritz, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
Wyllie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers,
'Y', Peterson, B., Swaller, T., Gibbons, M., Pape, D., Allevy, N., Schurk,
'R', Rittler, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann,
'R', Waterston, R. and Wilson, R.
Public Soybean EST Project

TITLE

JOURNAL

COMMENT

Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
High quality sequence stop: 412.
Location/Qualifiers

FEATURES

source

1. 498
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl055-4578"
/clone_11b="Gm-cl055"
/tissue_type="Mature seed pods, greenhouse grown"
/lab_host="DH10B"
/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI. The cDNA library was constructed from mRNA isolated
from mature seed pods of greenhouse grown plants prior to
senescence for the cultivar KPI. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments
were transformed into DH10B host cells (GibcoBRL). This
library was constructed in the laboratory of Dr. Randy
Shoemaker."

BASE COUNT 136 a 83 c 107 g 172 t

ORIGIN

alignment_scores:

Quality: 385.00 Length: 160

Ratio: 3.500 Gaps: 4

Percent Similarity: 68.750 Percent Identity: 49.375

alignment_block:

US-09-530-209a-2 x BG726093

Align seg 1/1 to: BG726093 from: 1 to: 498

72 LeuAspLeuAsnVa1G1yArGaSPaLaLeuAsnTrp1leTrpLysAl 88
|||||
3 TTGGACTTGGAGTCTT...AGGAAGAGGCTCTTGGATGGATTGGAGGCG 49
88 acyGluValHISGlnPheGlyProLeuCySPheCySLeuAlaMetAsp 105
| | | | |
50 TCATGCATTTGCTTGGACCTGCTGACCTTATGCTATGCTGTTAACT 99
105 yLeuAspArpPheLeuSerValHISAspLeuProSerGlySLyGlyTrp 121
|||||
100 ACTTGATGCTGCTTCATCATCATGATGATGATGATGATGATGATGATG 149
122 TleuGlnLeuLeuAlaVala1aCySLeuSerLeuAlaLys1leG1 138
|||
150 AGTATGCACCTGTTAGCTGTACGCTTGTCAATTCCTCCAAATGGA 159
138 uGluThrGluValProMetLeuLeuAspLeu.Gln..... 149
200 GGAAGATTAAAGTCCCTCTTGTGTAGATTACAGATTAGTACATCTTA 249
149 149
250 CTACCCAGATTTGCAATATATCTTTGGGTGGCATCTACATTTCTCTC 299
150ValGlyAspProGlnPheV 156
300 TGATTTTATCATCTTTGTTTGTATTGTTGTTGGTGAACCTAAAGTTTG 349
156 alPheGluAlaLysSerValGlnArGmetGluLeuValLeuAsnLys 172
350 CATTTGAAGCTAAAGACATTCAAAGATGACACTGCTGTAAAGACA 399
173 LeuLysTrpArGLeuArGAla1leThrProCySerTyrlleArGlyTrp 189
400 TTGAGATGGAAGAAATGCAAGCTTCACATTCATTTCCCTCCTAGATTACTT 449
189 eLeuArGlyMetSerLysCySAspGln 198
|||||
450 CCTCAGGAGAGATCACT...TGTGACCNA 474

seq_name: gb_est1:AI728767

seq_documentation_block:

LOCUS AI728767 512 bp mRNA EST 11-JUN-1999
DEFINITION BNLGH11561 Six-day cotton fiber Gossypium hirsutum cDNA 5' similar
to (AJ011892) cyclin D2.1 protein [Nicotiana tabacum], mRNA
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Gossypium hirsutum
upland cotton.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
1 (bases 1 to 512)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Ben Burr
Biology Department
Brookhaven National Laboratory
Upton, NY 11973, USA
Tel: 516-344-3396
Fax: 516-344-3407
Email: burr@bnl.bnl.gov
Seq primer: T3 Primer.

FEATURES

source

1. 512
/organism="Gossypium hirsutum"

/cultivar="Acala Maxxa"
 /db_xref="taxon:3635"
 /clone_lib="Six-day Cotton fiber"
 /tissue_type="Immature fiber"
 /dev_stage="Six days post anthesis"
 /lab_host="XLI-Blue"
 /note="Vector: pBluescript II KS+"

BASE COUNT 146 a 86 c 113 g 167 t
 ORIGIN

alignment_scores:

Quality: 369.50 Length: 172
 Ratio: 3.213 Gaps: 7
 Percent Similarity: 66.860 Percent Identity: 49.419

alignment_block:

US-09-530-209a-2 x AT728767 ..

Align seg 1/1 to: AT728767 from: 1 to: 512

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4  GUAsnleuGluLeuSer.....LeuLeuGysThrGlu..... 14
   ::::::::::: ||| |||||||:::
3  AAAAATCTGATTGTTCCACCTCAATCTCTCTGTGAGAGACGCAAG 52
   |||
15 .SerAsnValAspAspGlu.....GlyM 22
   |||
53 TCTCTGCTTGATGATGATCTGATTTAATCCATTAAGAGAGTTGGCG 102
   ::|
22 eTtLeValasp.....Glu 26
   ::|
103 TTTCCTCCGTATGTGACACGACCACTTAAACCAATCTTTAATCAACA 152
   |||
27 ThrProLeuGluLeuSer.....IleProGluMetGlu 37
   |||
153 GACCTCTTTTCATTAACACGATCACTATTGATGGGTAGTCTGG 202
   |||
37 yPheSerGlnSerGluSerGluGluIleIleMetGluMetValGluysG 54
   |||
203 TTTTCCA...ATACAAAGTATGATGATCAAGATCAAGAGATGTTGAAAAG 249
   |||
54 TULysGlnHisLeuProSerAspAspTyrTyrIleLysArgLeuArgSerGly 70
   |||
250 AGGTGAGACATTTGGCTGAAGATGATATATCTCAAGAGACTGAGAAAGTGGG 299
   |||
71 AspleuAspleuAsnValGlyArgArgAspAlaLeuAsnTrrPleTrrPly 87
   |||
300 GATTTGGCTTGAGTGT...ACGAAAGAGGCTCTTGATTTGATTTGCAA 346
   |||
87 salAcysGluValHisGlnPheGlyProLeuGysPheCysLeuAlaMet 104
   |||
347 GCTCTTCCTTATTACGTTTGGACCTTGAGCTTTGGCTTATCCATTA 396
   |||
104 snTyrLeuAspArgPheLeuSerValHisAspleuProSerGlyLysGly 120
   |||
397 ACTACTTGATCGGCTCTTCACTTATGACTTACCTACAGCTTAACA 446
   |||
121 TrrPleLeuGlnLeuAlaValAlaCysLeuSerLeuAlaLysIle 137
   |||
447 TGGACCTGCAATTTGCTGTGCTTTGTTTATCAATGACAGCAAAAT 496
   |||
137 egluGluThrGluVal 142
   |||
497 GGAGAGACAAAAGTT 512

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seq_name: gb_est1:AW042725

seq_documentation_block:

LOCUS AW042725 596 bp. mRNA EST 18-SEP-1999
 DEFINITION ST24F07 Pine tripleX shoot tip library Pinus taeda cDNA clone
 ACCESSION AW042725
 VERSION AW042725.1 GI:5903254

KEYWORDS

EST.
 loblolly pine.
 Pinus taeda

SOURCE

Pinus taeda

ORGANISM

Pinus taeda

REFERENCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.

AUTHORS

1 (bases 1 to 596)

TITLE

Whetten, R.W., Kinlaw, C.S., Retzel, E. and Sederoff, R.R.

JOURNAL

The Pine Gene Discovery Project

COMMENT

Unpublished (1999)

FEATURES

Forest Biotechnology Group
 North Carolina State University
 Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh
 NC, 27695-8008
 Tel: 919-515-7800
 Fax: 919-515-7801
 Email: rosswhetten@ncsu.edu

source

Location/Qualifiers
 1..596
 /organism="Pinus taeda"
 /db_xref="taxon:3352"
 /clone="ST24F07"
 /clone_lib="Pine TripleX shoot tip library"
 /lab_host="E. coli BM25.8"
 /note="Organ: shoot tips; Vector: Lambda Triplex; Site: 1:
 sfil (A); Site: 2: sfil (B); Shoot tips (approx. 2 cm from
 apex) were collected during the spring, frozen and used
 for mRNA isolation. The SMART-PCR method (Clontech) was
 used to prepare a library from 1 ug total RNA, using the
 Lambda Triplex vector. Plasmid subclones in pTriplex were
 recovered by cre-lox excision in E. coli strain BM25.8 and
 sequenced from the 5' end."

BASE COUNT 135 a 152 c 153 g 151 t 5 others
 ORIGIN

alignment_scores:

Quality: 366.50 Length: 200
 Ratio: 2.637 Gaps: 4
 Percent Similarity: 69.500 Percent Identity: 41.500

alignment_block:

US-09-530-209a-2 x AW042725 ..

Align seg 1/1 to: AW042725 from: 1 to: 596

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102 AlameTasnTyrLeuAspArgPheLeuSerValHisAspleuProSerG 118
   ::::::::::: ||| |||||||:::
10 TCTATAACTATCTAGATCGGTTTCTGTCCAGGAATCCACTACCGAAGC 59
   |||
118 yLysGlyTrrPleLeuGlnLeuAlaValAlaCysLeuSerLeuAla 135
   |||
60 CAAGCTCTGATGCTGCGACGCTCATCTGTGCTTGGCTTCTCTGCTG 109
   |||
135 lalysIleGluThrGluValPrometLeuIleaspleuGlnValGly 151
   |||
110 CTAAATAGAGAAACCAAGCTTCTTACTCTCGGACTTCGACGCGAA 159
   |||
152 AspProGlnPheValPheGluAlaLysSerValGlnArgMetGluLeu 168
   |||
160 GAGCCGCACTCTCTTGCAGCCGCTACTATCCAAAGATGAGCTTCT 209
   |||
168 uValLeuAsnLysLeuYstrPargLeuArgAlaIleThrProCysSer 185
   |||
210 GGTTCGTGACACTCTGGAATGGCGGATCTCTCTTACACCGTTTTCG 259
   |||
185 yTrleArgTyrPheLeuArgLysMetSerLysCysAspGlnGluProser 201
   |||
260 TCGTCATTTACTTCTTCAGGTT...GGAGGGGNGANGGCCAGCGCG 306
   |||
202 AsnThrLeuIleSerArgSerLeuGlnValIleAlaSerThrThrLysG 218
   |||

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307 AGAGCTATGCTGGCGGACCAATGAGCTCATATTCACACACACACACT 356
218 yliaaspheleugluPheargProsergluAlaAlaAlaValAlaL 235
357 GTTGGATTCTCTGAGCACCAGCATCTGCATATGCTGCGAGCTGTA 406
235 euserValsergluLeu.....GlnArgValHisPheASP 247
407 TCTGTCACTCCGAGAGCTTTGCCCTCGAAGACGACGACAGAGAC 456
248 AsnSerSerPheSerProleu..... 254
457 CAT.....CCTCTCTGCTCTCTGTAATAAAGATGGGTGT 494
255 .....PheSerLeuGlnLysGlnArgValLysLysIleGlyGln 269
495 CGGNTCCTATAGTCTGATACAGACTCTGATTGAGAAATCCGAGCC 544
269 etlleGluSerAspGlySerAspLeuCyserGlnThrProAsnGlyVal 285
545 TACACAGAAATCAATCAATCCTCTCATCCGACANAGCCTGTTGAGTG 594

seq_name: gb_est2:BG597062

seq_documentation_block:
LOCUS BG597062 728 bp mRNA EST 12-APR-2001
DEFINITION EST495740 csts Solanum tuberosum cDNA clone csts16p1 5' sequence,
ACCESSION BG597062
VERSION BG597062.1 GI:13615202.
KEYWORDS EST.
SOURCE potato.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 728)
REFERENCE van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chiemingo,A.,
AUTHORS Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.
TITLE Generations of ESTs from sprouting potato eyes
JOURNAL Unpublished (2000)
COMMENT Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdnaresgen.com
Seq primer: M13F-R.
FEATURES
source
Location/Qualifiers
1..728
/organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="csts16p1"
/tissue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
/note="vector: pBluescript SK(+); Site1: EcoRI, Site2:
XhoI; Various sizes of sprouting eyes (2mm to 15mm) were
taken from tubers. The tubers were incubated at 26C in the
dark for 2-3 weeks prior to sprouting. The eyes were
frozen in liquid nitrogen immediately upon removal from
tubers."
BASE COUNT 183 a 178 c 144 g 223 t
ORIGIN

```

```

Align seg 1/1 to: BG597062 from: 1 to: 728
10 LeuLeuCyThrIu.....SerAsnValAspAspG1 20
116 CTACTCTGGCGGAGACATCCGATACCGTTTCTCAACGAGAGAGAGA 165
20 uGlyMetIleValAspGluThrProIleGluIleSerIleProGluMetG 37
166 G.....GATTGCCGGAATGTT 182
37 LysPheSerGlnSerGluSer.....GluGluIleIleMet 48
183 CCTCGTCGGATATCGAATCTCACTTCGCGATATCGATGAATCAATCGCC 232
49 GluMetValGluLysGluLysGlnHisLeuProSerAspPylIlely 65
233 GGTCTTATCGAAGATGAGAAATTCGTACCTGGATTGACTATATCGA 282
65 sArgLeuArgSerGlyAspLeuAspLeuAsnValGlyArgArgAspAla 82
283 GAAATTCATCTCAATCTCTTAAGCGC...GCCGCTAGAGATGATCCG 329
82 euAsnThrPileThrPylAspAlaCysGluValHisGlnPheGlyProLeuGly 98
330 TTGCATGAGATTCTCAAGGTACAGCGCAGCATATGTTCCAGCCATTAAAG 379
99 PheCysLeuAlaMetAsnThrLeuAspArgPheLeuSerValHisAspLe 115
380 GCGTATCTCGCCGCTTACTATTCGATCGTTTCTCTACTCGAGAACTT 429
115 uproSerGlyLysGlyThrPileLeuGlnLeuAlaValAlaCysLeuS 132
430 GCGGCAAAACAATGGCGGCGGACTCAACTATGTCGGTGGCTGCTAT 479
132 erLeuAlaAlaLysIleGluGluThrGluValProMetLeuIleAspLeu 148
480 CTTTAGTGTGAAAAATGAGAGAACCTCTGTCTCTCTCTTTGGATCTT 529
149 GluValGlyAspProGlnPheValPheGluAlaLysSerValGlnArgMe 165
530 CAGGTGAAGGTGCGAAGTATATATTGAACCAAAACTATCCAAAGAT 579
165 tGluLeuLeuValLeuAsnLysLeuLysTrpArgLeuArgAlaIlehrp 182
580 GGAGTTCTTGTGCTGAGATTAAGATTGAGAGCGCTCCGATTAACCTC 629
182 rCysSerTrpIleArgTrpPheLeuArgLysMetSerLysCysAspGln 198
630 CGTTTACCTTCCTCAGCTTCTTTCGACCTAAACTGATTCACTAAGAACT 679
199 GluProSerAsnThrLeuIleSerArgSerLeuGlnValIle 212
680 TTCACCTGCT...TTCCTTATCTCAAGGCGTTCACAGATTATTC 718

seq_name: gb_est1:AI728683

seq_documentation_block:
LOCUS AI728683 562 bp mRNA EST 11-JUN-1999
DEFINITION BNLGH11316 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar
to (AJ011892) cyclin D2.1 protein [Nicotiana tabacum], mRNA
sequence.
ACCESSION AI728683
VERSION AI728683.1 GI:5047535
KEYWORDS EST.
SOURCE upland cotton.
ORGANISM Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
REFERENCE 1 (bases 1 to 562)
AUTHORS Blewitt,M., Matz,E.C., Davy,D.F. and Burr,B.
TITLE ESTs from developing cotton fiber

```

JOURNAL unpublished (1999)
 COMMENT Contact: Ben Burr
 Biology Department
 Brookhaven National Laboratory
 Upton, NY 11973, USA
 Tel: 516-344-3396
 Fax: 516-344-3407
 Email: burr@bnl.bnl.gov
 Seq primer: T3 Primer.

FEATURES
 source Location/Qualifiers
 1..562
 /organism="Gossypium hirsutum"
 /cultivar="Acala Maxxa"
 /db_xref="taxon:3635"
 /clone_lib="Six-day Cotton fiber"
 /tissue_type="immature fiber"
 /dev_stage="Six days post anthesis"
 /lab_host="XLI-Blue"
 /note="Vector: pBluescript II KS+"

BASE COUNT 156 a 101 c 117 g 186 t 2 others
 ORIGIN

alignment_scores: Quality: 362.50 Length: 175
 Ratio: 3.208 Gaps: 5
 Percent Similarity: 64.571 Percent Identity: 44.571

alignment_block:
 US-09-530-209A-2 x A1728683 ..

Align seg 1/1 to: A1728683 from: 1 to: 562

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4  Gtuasnlengluleuser.....leucocythrghuser.... 15
   |||||.....|
44  GAAATCTTGACTGTTCACCACTCAATCTTCTGTTGTGACACACAG 93
15  ..... 15
94  CTTCTGCTTGATGTGATCTGATTTTATGCTTGACGAGTTGGGG 143
16  ..... 16
144  CTTCCGTCCTTGTCATCACTCTTTAAACCAATCTTTATTCCAAT 193
19  AspGluglymetlleValaspglutThrProilegluileserleProgl 35
   |||.....|
194  GACCCCTTCTTATAACACAGATCACTCTTTCATGGGTTCCT.. 241
35  nmetglypheserGlnserGlnserGlnleilemetGluMetValG 52
   |||||.....|
242  ....GTTTTTGA...TTACAAAGTGATGATGATTAATTAAGCAATGGTTG 284
52  LuylsglyluysglnHlsleuproserAspAspTyrilleysArgleuArg 68
285  AAAAAGAGATGAGCATTTTGCCAGAGATGATTATCTTAAGACACTGAGA 334
69  SerGlyAspleuaspleuasnValGlyArgArgAspAlaLeuasnTrpI 85
   |||||.....|
335  AGGAGGAGATTGGAGTTGAGC...GCCAGAGAGAGGCTATTGGAATGAT 381
85  eTrpLysAlaCysGluValHlsGlnphGlyProleucCysPheCysLeu 102
   |||||.....|
382  TTGGAGCTTCANCTTATTTCATTTTGACCTGTGAGTCTTTGGCTAT 431
102  lAelAenTyrLeuAspArgPheLeuSerValHlsAspleuProSerGly 118
   |||||.....|
432  CCATTAACCTACTTGATCGGTTCCTTANCAATGATGATTACTAGAGGT 481
119  LysGlyTrpIleleuglnleuLeuAlaValAlaCysleuSerleuAla 135
   |||.....|
482  AAAACATGAGACTGTCCAACTTGCCGCTTGACATGTTTATCTATTGAC 531

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135 alysiilegluGluThrGluValPro 143
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 532 TAAATGAGAGAAACAAAGTGCT 556

seq_name: gb_EST:BG886881

seq_documentation_block: 749 bp mRNA EST 30-MAY-2001
 LOCUS BG886881
 DEFINITION EST512732 cSTD Solanum tuberosum cDNA clone cSTD214 5' sequence.
 mRNA sequence.
 BG886881

ACCESSION BG886881.1 GI:14263967
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 1 (bases 1 to 749)
 van der Hoeven, R., Bezzerides, J., Ewing, E., Cho, J., Chelmingo, A.,
 Bougri, O., Buell, C. R., Ronning, C., Tanksley, S. and Baker, B.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Unpublished (2001)
 Contact: Cathy Ronning
 The Institute for Genomic Research
 For clone info: please contact Research Genetics, Libraries
 Division tel 1-800-711-6195, email cda@resgen.com
 Seq primer: M13p-R.

FEATURES
 source Location/Qualifiers
 1..749
 /organism="Solanum tuberosum"
 /cultivar="Kennebec"
 /db_xref="taxon:4113"
 /clone="cSTD214"
 /clone_lib="cSTD"
 /tissue_type="dormant tuber"
 /dev_stage="one month post-harvest"
 /lab_host="SOLR"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
 XhoI; This library targets genes expressed in dormant
 tubers. This library was made from sections of dormant
 tuber, avoiding the buds and epidermis. Tubers were stored
 for one month post-harvest at 4oc. The tuber was peeled,
 well away from the surface. Then it was chopped into 1-2
 mm cubes and immediately frozen in liquid nitrogen. This
 library is noted as p4 in Tanksley lab notebooks."

BASE COUNT 197 a 181 c 146 g 225 t
 ORIGIN

alignment_scores: Quality: 360.00 Length: 187
 Ratio: 2.791 Gaps: 2
 Percent Similarity: 68.984 Percent Identity: 44.385

alignment_block:
 US-09-530-209A-2 x BG886881 ..

Align seg 1/1 to: BG886881 from: 1 to: 749

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78  ArgArgAspAlaLeuAsnTrpIleTrpLysAlaCysGluValHlsGlnph 94
   |||.....|
34  AGAGTGAATCCGTTGCATGATGATCTCAAGTACACAGCCCATGTGTTT 83
94  eGlyProleucCysPheCysLeuAlaMetAsnTyrLeuAspArgPheLeu 111
   |||||.....|
84  CCAGCATTAACGGCGTATCTCGCCGTTAACTATTCATGATGTTTCTCT 133
111  eValHlsAspleuProSerGlyLysGlyTrpIleleuglnleuLeuAla 127
   |||||.....|
134  ACTCGAAGACTTCCGCCAACAAATGCTGCGCCACTTCAACTATGTGCG 183
128  ValAlaCysleuSerleuAlaAlaLysIleGluGluThrGluValPro 144

```

```
|||||
184 GTTGCTGCTTACTTACGACAAATGAGAGACCTGTGTCCTTC 233
144 tleuileaspLeuGlnValGlyAspProGlnPheValPheGluAlaLysS 161
234 CCTTTGGATCTTCAGTGAAGGCCCAAGATATATATTGAAACCAAAAA 283
161 erValGlnArgMetGlnLeuValLeuAsnLysLeuLysTrpArgLeu 177
284 CTATCCAAAGAAATGGAGTTCTTGTAAGGATATTAGATTGAGAGCTC 333
178 ArgAlaIleThrProCysSerTyrIleArgTyrPheLeuArgLysMetSe 194
334 CGATCCATAACTCCGTTTAGCTTCCTCAGTTCTTGCAGGCTAAACTGA 383
194 rLysCysAspGlnGluProSerAsnThrLeuIleSerArgSerLeuGlnV 211
384 TTCACCTAGGAACCTTCACCTGCG...GTCCCTATATCAAGGCGCTTCAGA 430
211 alIleAlaSerThrThrLysGlyIleAspPheLeuGlnPheArgProSer 227
431 TTATCTCTCTATATATTCAAGAACTAGCTTTCATGAGTATTGCCATCA 480
228 GluAlaIleAlaValAlaLeuSerValSerGlyGlnLeuGlnArgVa 244
481 TGCATAGCTGCACACTACATACTATGTGCAGCTAAGACCTT..... 522
244 lHisPheAspAsnSerSerPheSerProLeuPheSerLeuLeuGlnLysG 261
523 .....CCAAATTCTCTCTTGTGATGCTG 547
261 luArgValLys 264
548 AACATGCTGAA 558
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 30, 2002, 11:05:26 ; Search time 1389.93 Seconds
(Without alignments)
11061.975 Million cell updates/sec

Title: US-09-574-735C-1

Sequence: 1 ggcacgagagagaccacaa.....ttaataactaagtattat 932

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
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34: gb_pat:*
35: gb_ph:*
36: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	932	100.0	932	6 A98054	A98054 Sequence 1
2	842.8	90.4	855	6 A98054	A98054 Sequence 1
3	744.8	79.9	755	6 A98054	A98054 Sequence 1
4	660.2	70.8	841	6 A98054	A98054 Sequence 1
5	54.2	8.2	7218	6 A98054	A98054 Sequence 1
6	54.2	5.6	6660	6 A98054	A98054 Sequence 1
7	52.2	5.6	856	6 A98054	A98054 Sequence 1
8	52.2	5.6	904	6 A98054	A98054 Sequence 1
9	51.8	5.6	1141	6 A98054	A98054 Sequence 1
10	51.4	5.5	443	6 A98054	A98054 Sequence 1
11	50.6	5.4	15892	6 A98054	A98054 Sequence 1
12	50.6	5.4	83365	6 A98054	A98054 Sequence 1
13	50.6	5.4	213467	6 A98054	A98054 Sequence 1
14	50.6	5.4	377	6 A98054	A98054 Sequence 1
15	49.8	5.3	51952	6 A98054	A98054 Sequence 1
16	49.8	5.3	51952	6 A98054	A98054 Sequence 1
17	49.8	5.3	51953	6 A98054	A98054 Sequence 1
18	49.8	5.3	71327	6 A98054	A98054 Sequence 1
19	48.6	5.2	2290	6 A98054	A98054 Sequence 1
20	48.6	5.2	43814	6 A98054	A98054 Sequence 1
21	48.6	5.2	73345	6 A98054	A98054 Sequence 1
22	48.6	5.2	171842	6 A98054	A98054 Sequence 1
23	47.8	5.1	1233	6 A98054	A98054 Sequence 1
24	47.8	5.1	2924	6 A98054	A98054 Sequence 1
25	47.8	5.1	152237	6 A98054	A98054 Sequence 1
26	47.8	5.1	164399	6 A98054	A98054 Sequence 1
27	47.6	5.1	38702	6 A98054	A98054 Sequence 1
28	47.6	5.1	41305	6 A98054	A98054 Sequence 1
29	47.6	5.1	85757	6 A98054	A98054 Sequence 1
30	47.6	5.1	92633	6 A98054	A98054 Sequence 1
31	47.6	5.1	321003	6 A98054	A98054 Sequence 1
32	47.4	5.1	3240	6 A98054	A98054 Sequence 1
33	47.4	5.1	3240	6 A98054	A98054 Sequence 1
34	47.2	5.1	10176	6 A98054	A98054 Sequence 1
35	47.2	5.0	2305	6 A98054	A98054 Sequence 1
36	47.2	5.0	6872	6 A98054	A98054 Sequence 1
37	47.2	5.0	11166	6 A98054	A98054 Sequence 1
38	46.8	5.0	192929	6 A98054	A98054 Sequence 1
39	46.8	5.0	256172	6 A98054	A98054 Sequence 1
40	46.6	5.0	1838	6 A98054	A98054 Sequence 1
41	46.6	5.0	4163	6 A98054	A98054 Sequence 1
42	46.6	5.0	8574	6 A98054	A98054 Sequence 1
43	46.6	5.0	153098	6 A98054	A98054 Sequence 1
44	46.4	5.0	302	6 A98054	A98054 Sequence 1
45	46.4	5.0	844	6 A98054	A98054 Sequence 1

ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	REFERENCE	TITLE	JOURNAL	FEATURES	CDS
1	A98054	Sequence 1 from Patent WO9914331.	A98054	A98054	GI:6781292	unclassified.	De A.J. and De V.L.	CYCLOIN-DEPENDENT KINASE INHIBITORS AND USES THEREOF	ALMEIDA JANICE DE (BE); LANDRIEU ISABELLE (BE)	Location/Qualifiers	
						unclassified.				1. 932	
						unclassified.				/organism="unclassified"	
						unclassified.				/db_xref="taxon:32644"	
						unclassified.				86. 715	

Db 121 TCTCCGTGTACACGCGACGAAATCGCGGTGGAATTTGCGGAGAAATTCAGCAGGAGCG 180
 QY 266 tcggaagacagtgctgtttagtagcagcgagatcttcctccggttaagaacagtg 325
 Db 181 TCGGAGACGAGTGTGTATAGACGCGCGGATTCCTCGGTTGAAGAACAGTGT 240
 QY 326 caaatcgaagaagaagatcgcgtgcttgcgtgtgttctacatcgaagaagaatcgaa 385
 Db 241 CAATCGAAGAAGAAATCGTCGCTTGTGTGTCTACATCGGAGAGAAATCGAAA 300
 QY 386 cggagaatcgaattgttagactcttgagaaataacggtgacgtctgtaaacagaacg 445
 Db 301 CGGAGAAATCGAATTTGTAGATCTTGAGAAATAACGATGACATCGTGAACAGAAACG 360
 QY 446 tctgtgattcagagattgaaataagaatgagaaatcgatgaaatcgatcttcctcg 505
 Db 361 TCGTGATTATGAGATGATTTGAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 420
 QY 506 gtgagctgtgaagatgtagagctgcgcaaggttaagaagaagatcgcagagcgctg 565
 Db 421 GTGCGCTGTGAAGATGATGAAGTCTCGCCGAGGTGAAGAGAGTCTCCATGAGAGCGTG 480
 QY 566 aaggaagctgagttagaagaatttttcaggtgagcgagaaagatctcgaaataagtg 625
 Db 481 AAGGAAGCTGAGTTAGAACACTTTTTCAGGTGCGGAGAAAGATCTTGGAATTAAGTTG 540
 QY 626 ttggaatgttcatgagataaactcgcgttccgagaagaatgagcaactgtgtgagga 685
 Db 541 TTGGAATGTCTATGAAGATTAACCTTCGATTCGAGAAAGATGAGCACTTGTTGAGGA 600
 QY 686 agataagctgagttgaatgaatcgaataagaagaagaatgagatgaatgagatgag 745
 Db 601 AGATACGAGATGGGTAAATTTGAATCCATGAGAGAGCGATGATGAATGAATGATGATG 660
 QY 746 ttcccaagaatcactatattttctctgtgaataactctgtctgattttctt 805
 Db 661 TTTTACCAAGACTTATTAATTTCTCTGTGAATTAATCTTGTGATTTTCTTTT 720
 QY 806 aacaaatccaaatgtagatattcttctcgcgaataaataaataaactt 865
 Db 721 AACAAATCCAAATGATGATCTCTCTCGAATTAATCAATTAATCAATCAATCAAT 780
 QY 866 ttgttactctctgaggttaataatgagatcgtgttcttcgatttaataaactata 925
 Db 781 TGTTTACTTCTCTGAGGTAATTAATTAATTAATTAATTAATTAATTAATTAAT 840
 QY 926 agtta 931
 Db 841 AGTTTA 846

 RESULT 3
 AX008796 755 bp DNA PAT 06-SEP-2000
 LOCUS AX008796
 DEFINITION Sequence 6 from Patent WO964599.
 ACCESSION AX008796
 VERSION AX008796.1 GI:9996260
 KEYWORDS
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 1 (bases 1 to 755)
 REFERENCE
 1 Fowle, L.C., Wang, H. and Crosby, W.L.
 Cyclicin-dependent kinase inhibitors as plant growth regulators
 Patent: WO 964599-A 6 16-DEC-1999;
 FOWLE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD
 (CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV
 SASATCHEMAN TECHNOLOGIES (CA)
 FEATURES
 source Location/Qualifiers
 1..755
 /organism="Arabidopsis thaliana"

BASE COUNT 229 a 106 c 187 g 233 t
 ORIGIN
 Query Match 79.9%; Score 744.8; DB 6; Length 755;
 Best local similarity 99.7%; Pred. No. 1.8e-146;
 Matches 746; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 QY 185 gtggaatcaggaatattctgtctccgtgtgtacagcgagaaatcggtggaattgt 244
 Db 1 GTGGAATCTAGGATTAATTTGTCCTCGTGTGTACAGCGCGAATCGCGGTGAATTTGT 60
 QY 245 gggagaatttcagcaagcgctgtgagagagtggttagtagtaagcgagagattcg 304
 Db 61 GCGAGAAATTCACAGAGCGCTGAGACGAGTGTGTATAGTACGACGCGAGATTTCT 120
 QY 305 cctcggttgaagaacagtgctcaaatcgaagaagaagatcgcgtgttcgtgtctct 364
 Db 121 CTTCCGTTGAAGACAGTGTCAATCGAAGAGAAATTCGCGGTTTCTGTTCTTCT 180
 QY 365 acatcggaagaagaatcgaaacggagaatcgaaattgtgagatctgaggaataaagct 424
 Db 181 ACATCGGAAGAGAAATCGAAACGAGAAATCGAATTTGTAGATCTTGAGAAATTAACG 240
 QY 425 gacgactggaagaacagaacagctgtgtatttagagattgaaatgaagtgaagatcg 484
 Db 241 GACGATCGTCAAAACAGAAACGCTGTGATTTACGATGATTTGAATGAAGTGAAGATTCG 300
 QY 485 atgaacatgagatctctctcgtgtgtgtgaaagatgagatcgcgcgaagttaag 544
 Db 301 ATGAACATGATTTCTTCTCGTGTGCTGTTGAAGATGTAGTCTGCGCCAGATTAGC 360
 QY 545 aagagctccatgagaacggtgagaagagctgagttgagaatttttccaagtgcgag 604
 Db 361 AAGAGTCTCATGAGACGAGGAGAGAACTGAGTGAAGAACTTTTTCAGTGGCGGAG 420
 QY 605 aagaatcttcgagaataagtggtgtgagatgtctatgaagataacttcgattcgaga 664
 Db 421 AAGATCTTCTGGAATGAATGTTGGAATGTTCTATGAAGATTAATCAATTCGATTCGAGAA 480
 QY 665 gatgagcaactgtgtgagaagatacgagtggtttaaatgtgatacgaataagaagcga 724
 Db 481 GATGAGCACTTGTGTGAGAGAAATGAGACTGGGTTAAATGCAATGAAGAAAGCA 540
 QY 725 tgaataatgataatcattgtttccacaaagtaactaattttcttcgtaaat 784
 Db 541 TGATGAATATGATGATCATGTTTTCACCAAGTACTTATTAATTCCTGTAATAT 600
 QY 785 ctgtgttgaattttctttaaacaataccaatgaatgaatcttctcgaataatc 844
 Db 601 CTTTGTCTGATTTTCTTTTAACAAATCCAAATGATGATCTTCTTCGAATATATC 660
 QY 845 aataacatgtaatacaactttgttgaatcctcgtgagtaataatgagatcgtgt 904
 Db 661 AATAACATGTAATTCAACTTTGTTGTACTTCTGAGGTAATTAATTAATTCGTTG 720
 QY 905 ttctcgatttaataaactaagttat 932
 Db 721 TTTCTCGATTAATTAATCAATTAATTAATTAATTAATTAATTAATTAATTAAT 748

 RESULT 4
 ATT345 84196 bp DNA PLN 26-JAN-2000
 LOCUS ATT345
 DEFINITION Arabidopsis thaliana DNA chromosome 3, BAC clone T345.
 ACCESSION AL132979
 VERSION AL132979.2 GI:6782244
 KEYWORDS
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

REFERENCE 1 (bases 1 to 84196)
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 AUTHORS Bloecker, H., Mewes, H.W., Lemcke, K., Mayer, K.F.X., Quetier, F. and Salanoubat, M.
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 84196)
 EU Arabidopsis sequencing project.
 AUTHORS Direct Submission
 TITLE Submitted (25-JAN-2000) MIPS, at the Max-planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemeckemips.bloecher.mpg.de, mayer@mips.biochem.mpg.de, Project Coordinator: Marcel Salanoubat and Francis Quetier, Groupe ment d'Interet Public, Centre National de Sequencage - GENOSCOPE, 2 rue Gaston Cremlieux, BP191, 91006 Evry Cedex, France;
 http://www.genoscope.cns.fr
 COMMENT On Jan 27, 2000 this sequence version replaced gi:6434247. Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
 FEATURES
 source Location/Qualifiers
 1. 84196
 /organism="Arabidopsis thaliana"
 /variety="Columbia"
 /db_xref="taxon:3702"
 /chromosome="3"
 LTR 2983..3338
 /note="355 bp LTR"
 3339..7564
 /note="LTR-transposon"
 7565..7922
 /note="367bp LTR"
 12339..13197
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 /gene="T3A5.10"
 /note="similarity to cyclin-dependent kinase inhibitor (ICK1), Arabidopsis thaliana, EMBL:AFU94772_1"
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 /product="putative protein"
 /protein_id="CAB62432.1"
 /db_xref="GI:6561966"
 /translation="MAAVRRRRDVEENGVTITTKRRKMEEDVLVESRTITLSPV
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 KKELEDFROVAEKDLRNKLLECSKYNDFEKDELGGREWEWKLP"
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 12666..12741
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 /number=1
 12742..12803
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 /number=2
 12804..12887
 /gene="T3A5.10"
 /number=2
 12888..13055
 /gene="T3A5.10"
 /number=3
 13056..13124
 /gene="T3A5.10"
 /number=3
 13125..13197
 /gene="T3A5.10"
 /number=4
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 /number=1
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 /gene="T3A5.20"
 complement(join(15858..15901,16014..16470))
 /note="similarity to predicted proteins, Arabidopsis thaliana"

/codon_start=1
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 /db_xref="GI:6561967"
 /translation="MARLEHNSMNGCARISFNSNEFVEIRSEKSNKNNINRSRSPS
 MPSADFAFVSVDYSMIPADEIFLKCKIIPFKETSHVHRIGELLTEEGSGVDSNTF
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 /number=2
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 HPPPPPPDPDNLQPIFKAIHDYAKRPETKPTLIRIKESVSGSDPIORGYPAE
 ALSHKEESPSSSSSSLEDFILSYRTLNDACTSKFAHITANQALILEATNOSNIHI
 VDFGIFQGIOWSALIQALATRRSSGKPTLRISGIPASGDSGPELITAGNLRDPA
 AILDNFEFVPLVPIQLNGSSFRVDPDEVLVNMLELYKLIDTATVGTALIA
 RSLNPRIVTIGEYEVSLNRYEFANRVKNSLREYSAYFESLEPMLDSDSERLVERVL
 FGRIMDLVSDDDNPGRRGLMEKEDQRYLMEKAGEPEYKPSNVASQAKLLM
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 26093..28999
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 complement(join(26093..26338,27091..27200,27308..27386,
 27478..27570,27723..28037,28136..28288,28374..28698,
 28779..28999))
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 signature AA435-464, Probkaryotic membrane lipoprotein lipid
 attachment site AA320-330"
 /codon_start=1
 /product="steroid 22-alpha-hydroxylase (DWF4)"
 /protein_id="CAB62435.1"
 /db_xref="GI:6561969"
 /translation="MFEETENHTLLPILLPSLISLILFLILKRNKTRFNPPLPKS
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 TLFVLDSSQOONSIFSAODEAKKFTFMRMARHIMSDGEETEDLKEIYTFKGVYS
 APLNLPCTAAYHKALOSRAITLKFIERKMEERKIDIKEDDEEVEVKTEDAESKSDH
 VRKORTDDDLIGWLTKHSNLSSTEOILDLILSLFAGHETSVAIALAIFLQACPKAV
 EELREHETIRAKKEIGESSELNMDVDYKKMDFTQCVINETLRIGNVYFLRRALKDV
 RYKGDIPSGKVLPIVISAHLDNSRVDQPLTFPMRMQOONNGASSGSGSPSTGNC
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 complement(26093..26338)
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 complement(27571..27722)
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 /number=5
 complement(28038..28135)
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source	1. .7218	/organism="unknown"
BASE COUNT	1944 a	1491 c
ORIGIN	1486 g	1929 t
		368 others

Query Match	8.28; Score 76.2; DB 6; Length 7218;
Best Local Similarity	6.58; Pred. No. 3.5e-06;
Matches 27; Conservative	235; Mismatches 153; Indels 0; Gaps 0;

[illegible]

RESULT	6
LOCUS	PfMAL13P6
DEFINITION	PFMAL13P6 204652 bp DNA HTG 19-AUG-1999 Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.
ACCESSION	AL049183
VERSION	AL049183.5 GI:5763804
KEYWORDS	HTG; HTGS PHASE1.
SOURCE	malaria parasite P. falciparum.
ORGANISM	Plasmodium falciparum
REFERENCE	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
AUTHORS	Bowman,S., Churcher,C., Harris,B., Harris,D., Lawson,D., Quail,M. and Barrett,J.
TITLE	Direct Submission
JOURNAL	Submitted (15-MAR-1999) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK
COMMENT	On Aug 24, 1999 this sequence version replaced gi:5731886.

FEATURES	Location/Qualifiers
source	1. .204652

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/organism="Plasmodium falciparum"
/strain="3D7"
/db_xref="taxon:5833"
/chromosome="13"
BASE COUNT 68880 a 17396 c 17710 g 67856 t 32810 others
ORIGIN

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Query Match	5.8%;	Score 54.2;	DB 2;	Length 204652;
Best Local Similarity	53.8%;	Pred. No. 0.17;		
Matches 133;	Conservative	0;	Mismatches 113;	Indels 1;
			Gaps	1;

QY	686	agatacaggttggttcaattcaaccatgaagaacgatcatatacatgacatg	745
Db	49307	ATATCCCAATTTTTTTTATATTATATATATAAAAAAGATTTGTATATATTTGATTAATAATG	493
QY	746	tttccaccaagaactaattattttctctcgtataatacttgcttgattttcttt	805
Db	49367	TGCGTCTTAAATTTTAA-TGTTTTCTTTCTTCATACAGTTTCTAAAAATTCGGTTAT	494
QY	806	aacaaatccaaatgtagatattcttcctcgcgaataacataacatgtaattcaactt	865
Db	49426	ATTAATTTCTTAAATATTCAGTACGATTTCTTTATTCACCAACATGGTCTTCATCAATAAT	494
QY	866	tgtttgtaacttccttgagtgatattatagattcgtgtttttctcgtataataacata	925
Db	49486	TATATGTACTAATTTGATGTATTAATAATCATATAGATTTTAATGACATMAAATTCGTATA	495
QY	926	agttat 932	
Db	49546	ATTTAAT 49552	

RESULT	7				
LOCUS	AX008793				
DEFINITION	AX008793	660 bp	DNA	PAT	06-SEP-2000
ACCESSION	AX008793	Sequence 3 from Patent WO964599.			
VERSION	AX008793.1	GI:996257			
KEYWORDS					
SOURCE	thale cress.				
ORGANISM	Arabidopsis thaliana				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
AUTHORS	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
TITLE	Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
JOURNAL	1 (bases 1 to 660)				
	Fowke, L. C., Wang, H. and Crosby, W. L.				
	Cyclin-dependent kinase inhibitors as plant growth regulators				
	Patent: WO 964599-A 3 16-DEC-1999;				
	FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANADA				
	(CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV				
	SASKATCHEWAN TECHNOLOGIES (CA)				
FEATURES	Location/Qualifiers				
source	1..660				
	/organism="Arabidopsis thaliana"				
	/db_xref="taxon:3702"				
BASE COUNT	232 a	66 c	186 g	176 t	
ORIGIN					

Query Match	5.6%	Score 52.2	DB 6	Length 660
Best Local Similarity	56.58	Pred. No. 0.34		
Matches 143	Conservative	0	Mismatches 98	Indels 12
	Gaps			
QY	557	gagcgcgtgaggaagctgagttgaagaatcttttcacgtgcgaggaagaatcttcg	616	
Db	379	GAGATGCCAAGCGATCGAAATTTGAAATTTTCTGCAACCTGAGAAACACCTCAA	438	
QY	617	aataagttgttggaatgtctctatgaataactgcattcagagaagaatgagccact	676	
Db	439	GAAATAATTCAG-----AGAGATACAAATTTCCATTTCAGAGAGGAGAACCCATTA	489	
QY	677	qqtcaagaagaatatacagttqqttaaatatgaatccatcaagaagaacatataataatga	736	

QY	Db	737	tgatcatgttttaccacaagtlactatatttctctcgttaataatccttgcttgat	796
Db	490	GA----	AGACACTTTCGATATGGCTAAAGTTAAGATGACAGACAAAGACAGAGATTATGGTTT	546
QY	737	tgatcatgttttaccacaagtlactatatttctctcgttaataatccttgcttgat	796	
Db	547	TTTTTTTAACCTTTTACATTATTATATTTCAGGGAATAAGTAATTATTATTGTTGATT	606	
QY	797	tttctcttcaaca	809	
Db	607	TGAAATATATAGA	619	
RESULT	8			
LOCUS	ATU94772	856 bp	mRNA	29-APR-1997
DEFINITION	Arabidopsis thaliana cyclin-dependent kinase inhibitor protein (ICK1) mRNA, complete cds.			
ACCESSION	U94772			
VERSION	U94772.1	GI:2052501		
KEYWORDS	thale cress.			
SOURCE	Arabidopsis thaliana			
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.			
REFERENCE	1 (bases 1 to 856)			
AUTHORS	Wang, H., Fowke, L.C. and Crosby, W.L.			
TITLE	A plant cyclin-dependent kinase inhibitor gene			
JOURNAL	Nature 386 (6624), 451-452 (1997)			
MEDLINE	97242401			
REFERENCE	2 (bases 1 to 856)			
AUTHORS	Wang, H., Fowke, L.C. and Crosby, W.L.			
TITLE	Direct Submission			
JOURNAL	Submitted (20-MAR-1997) Plant Biotechnology Institute, 110			
FEATURES	Gymnasium Place, Saskatoon, SK S7N 0W9, Canada			
SOURCE	Location/Qualifiers			
gene	1..856			
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	/strain="Columbia"			
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	7..582			
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	/product="cyclin-dependent kinase inhibitor protein"			
	/protein_id="AAC49698.1"			
	/db_xref="GI:2052502"			
	/translation="MVRKRAKGIYAGVSYTYMOAIRSRIVYVRKSSSVAGD			
	NGVSSSCSGSNEYKKKELIHDEEDKDGDETSTYRKQTRKLDENRDEEKELSKS			
	MEVNSFEESAIVKESLDCCSGRKTMEETVAEEERAKLMTPEPTESEIDFVEAE			
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BASE COUNT	292 a 92 c 225 g 247 t			
ORIGIN				
Query Match	5.6%	Score 52.2;	DB 8; Length 856;	
Best Local Similarity	56.5%;	Pred. No. 0.34;		
Matches 143; Conservative	0;	Mismatches 98;	Indels 12; Gaps 2;	
QY	557	gagacggtgaaggaagcgtgaattagaaatctttctcaggtgagcgagaagaatcttcg	616	
Db	439	GAGATGCCAACGACGATCGGAATTCGAAATTTTTTTTTTGTGGAGACTGAGAAACAACTCAA	498	
QY	617	aataagttgttcgaatgtctcatgaagatcaacttcgatttcgagaagaatgagccact	676	
Db	499	GAAAAATTCAG-----AAGACATGACATTTTCGATTCGAGAGAGAGAACCATTA	549	
QY	677	ggtgaggaagaatacgaatgtggttaaatgaatccatgaagaagaacgaatgataatga	736	
Db	550	GA---AGACCTTTACGATGGGTAAAGTTAGAGTGAAGAAGAAGAAGATTATGCTTT	606	
QY	737	tgatcatgttttaccacaagtlactatatttctctcgttaataatccttgcttgat	796	

Db	607	TTTTTTTACTTTTGTAGATTTAATATTATTTACAGGGAATAGTTAATTTATTTTGTGTTGATT	666
QY	797	ttttctttaaca 809	
Db	667	TGGAATATTAAGA 679	
RESULT	9		
AX008791			
LOCUS	AX008791	904 bp DNA	PAT 06-SEP-2000
DEFINITION	Sequence 1 from Patent WO9964599.		
ACCESSION	AX008791		
VERSION	AX008791.1	GI:9996235	
KEYWORDS			
SOURCE			
ORGANISM	thale cress. Arabidopsis thaliana		
REFERENCE	Arabidopsis: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 904) Fowke, L.C., Wang, H. and Crosby, W.L. Cyclin-dependent kinase inhibitors as plant growth regulators Patent: WO 9964599-A 1 16-DEC-1999; FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD (CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV SASKATCHEWAN TECHNOLOGIES (CA) Location/Qualifiers 1..904 /organism="Arabidopsis thaliana" /db_xref="taxon:3702" 55..630 /note="unnamed protein product" /codon_start=1 /protein_id="CAC07437.1" /db_xref="GI:9996235" /translation="MVRKRYKAKIVGASSTYMOLRRIYVRSKSSVSVCN NGVSSSGSNGEYKKEKLEHLEEDKDGDTSTYRYTKKLEPNEEKEKELSSK MENVSSFEESAVKESLDCCCGKRTMETETVAEEEEKAKLMTPESEIDFVEAE KOLKEKFKKKYNFPEKEKPLEGKYEYWKLE"		
BASE COUNT	307 a 107 c 229 g 261 t		
ORIGIN			
Query Match	5.6%; Score 52.2; DB 6; Length 904;		
Best Local Similarity	56.5%; Pred. NO. 0.34;		
Matches 143; Conservative 0; Mismatches 98; Indels 12; Gaps 2;			
OY	557	gagagcggtgaagaagcgtgagttaagaatcttttcagtggtgcgagagaagatcttcgg 616	
Db	487	GAGATGCGCCACGACGAAATCGAAATTTAAAGATTTTTTGTGGAAAGCTGAGAAACAACCTCAAA 546	
OY	617	aataagtcgttggaatggttcctagaatcgaatcactcgatctcgagaagaatgagccactt 676	
Db	547	GAAAAATTCACG-----AAGAAGTACAAATTTTCGATTTTGAGAGAGAGAAAGCCATTAA 597	
OY	677	gttgaggaagatacgaagtgggttaaatgaaatccatgaaagaagacgatgatgataatga 736	
Db	598	GA---AGGACGTTACGAATGGCTAAAGTTAGAGTGAAAGAAAGAAAGAAAGTTATGTTT 654	
OY	737	tgatcatcgtttcacccaagaactatattttctctcgtaaatcatcttgcttgat 796	
Db	655	TTTTTTTAACTTTTGTAGATTTTAATATTTTCAGGGAATAGTTAATTTTATTTGTTGATT 714	
OY	797	tttctcttaaca 809	
Db	715	TGGAATATTAAGA 727	
RESULT	10		
LOCUS	AX083744	1141 bp DNA	PAT 28-FEB-2001
DEFINITION	Sequence 22 from Patent WO0111061.		

ACCESSION AX083744 GI:13185472
VERSION AX083744.1
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 1141)
AUTHORS Kunst, L. and Clemens, S.
TITLE Regulation of embryonic transcription in plants
JOURNAL Patent: WO 011061-A 22 15-FEB-2001;
UNIVERSITY OF BRITISH COLUMBIA (CA)
FEATURES
source 1..1141
/organism="synthetic construct"
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promoter 1..1141
/note="consensus sequence of A.t., L.a., and B.n. PAEI
promoters"
BASE COUNT 123 a 32 c 42 g 112 t 832 others
ORIGIN
Query Match 5.6%; Score 51.8; DB 6; Length 1141;
Best Local Similarity 10.6%; Pred. No. 0.42;
Matches 83; Conservative 310; Mismatches 380; Indels 13; Gaps 2;
QY 130 tggagttacgaacgacggtgaacgaagatgaggaagatgagattagtgga 189
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QY 190 atcagaataatctgctcgtgtacagagcagaacatcggtgagatgagcga 249
DB 115 TNNKGTGRHRRWRARABDVTDDHHVTAMNNATWTTMCMDDDKRTRWKKNNATG 174
QY 250 aactcagcagagcgtcgcgaacgagctgtgtatagcagcagcagatctctcc 309
DB 175 WDDDTYYHMMNNNGCBTVWVRYKTRDMSBRMNYGMBWNNWSYDYVYVWVDDMC 234
QY 310 ggttgaagaacagtgctcaatcgaagaagaatgctggttctgtgtctacatc 369
DB 235 KRVVRRWVRKRGMMRYWAMBTARHRRYNGTBAATYRTWMMNNNNNAKMKRAKY 294
QY 370 ggaagaacatcgaacggaacatctgtatctgtgaagaacatcagtgagca 429
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QY 788 tggctgattcttcttcaacaatacgaatgtagatcttctcgtcgaataatc 847
DB 704 TRRTMKNNNNNAGTWKNNNNNNNAKASAKNYAAALVAAKAKHMKWANKMARGHAD 763

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QY 908 ctcgat 913
DB 824 VTMWAW 829
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LOCUS AX008794
DEFINITION Sequence 4 from Patent WO964599.
ACCESSION AX008794
VERSION AX008794.1 GI:9996258
KEYWORDS
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 443)
AUTHORS Fowke, L.C., Wang, H. and Crosby, W.L.
TITLE Cyclin-dependent kinase inhibitors as plant growth regulators
JOURNAL FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD
(CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV
SASKATCHEWAN TECHNOLOGIES (CA)
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Best Local Similarity 57.3%; Pred. No. 0.49;
Matches 138; Conservative 0; Mismatches 91; Indels 12; Gaps 2;
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DB 317 GA--AGGAGCTACGAATGCGTAAGTTAGAGTGAAGAAGAAGAGAGTATGTTT 373
QY 737 tgatcattgtttcaccagaactatatttttctcgtatataatcttgcattg 796
DB 374 TTTTCTTAACTTTTGAATTTAATTTTCAGGGAATAGTTAATTTTATTTGTTGATT 433
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DB 434 T 434
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LOCUS AE001419
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ACCESSION AE001419 AE001362
VERSION AE001419.1 GI:3845281
KEYWORDS
SOURCE malaria parasite P. falciparum.
ORGANISM Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

HTG.
thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi
1 (bases 1 to 83365)
Lin, X., Kaul, S., Rounsley, S.D., Shea, T.P., Benito, M.-I., Town, C.D.,
Fuji, C.Y., Mason, T.M., Bowman, C.L., Barnstead, M.E.,
Feldblyum, T.V., Buell, C.R., Ketchum, K.A., Lee, J.J., Ronning, C.M.,
Koo, H., Morfitt, K.S., Cronin, L.A., Shen, M., Vanaken, S.E., Umayam, L.,
Tallon, L.J., Gill, J.E., Adams, M.D., Carrera, A.J., Creasy, T.H.,
Goodman, H.M., Somerville, C.R., Copenhaver, G.P., Preuss, D.,
Niemann, W.C., White, O., Eisen, J.A., Salzberg, S.L., Fraser, C.M. and
Venter, J.C.
Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana
Nature 402 (6763), 761-768 (1999)
20083487
10617197
2 (bases 1 to 83365)
Lin, X.
Direct Submission
Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
On Dec 17, 1999 this sequence version replaced gi:4587677.
The sequence and annotation of chromosome 2 were merged from those
of the individual clones on this chromosome after removing
overlaps. For detailed information, please see the TIGR web site
(http://www.tigr.org/tdb/at.html).

Genes were identified by a combination of three methods: Gene
prediction programs including GRATL
(ftp://arthur.eppm.ornl.gov/pub/xgrat), Genefinder (Phil Green,
University of Washington), Genscan (Chris Burge,
http://genome.stanford.edu/GENSCAN.html), and NetPlantGene
(http://www.cds.dtu.dk/services/NetGene2/), searches of the
complete sequence against a peptide database and plant EST
databases at TIGR, and manual curations based on those analyses.
Annotated genes are named to indicate the level of evidence for
their annotation. Genes with similarity to other proteins are named
after the database hits. Genes without significant peptide
similarity but with EST similarity are named as 'unknown' proteins.
Genes without protein or EST similarity, that are predicted by two
or more gene prediction programs over most of their length are
annotated as 'hypothetical' proteins. Genes encoding tRNAs are
predicted by tRNAScan-SF (Sean Eddy,
http://genome.wustl.edu/eddy/tRNAScan-SF/). Simple repeats were
identified by repeatmasker (Arian Smit,
http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are
numbered from the top to bottom of the chromosome.

We thank the GSH/WashU/ABI consortium for sequencing BAC clones
P6P23, F536, T17A5, and T13L16, the ESSA group for sequencing clone
F1304, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards
and Satoshi Tabata for helpful assistance. In addition, we would
like to thank the TIGR Bioinformatics Department, especially Lixin
Zhou, Hanif Khalek, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy
Peterson, Michael Holmes, and Delwood Richardson for software and
database support.

This work was supported by the National Science Foundation,
Department of Energy and the US Department of Agriculture.

Address all correspondence to: atettigr.org.
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Matches 104; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

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LOCUS
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DEFINITION
Homo sapiens chromosome 2 clone RP11-480a6, WORKING DRAFT SEQUENCE,
9 unordered pieces.
ACCESSION
AC016912
VERSION
AC016912.5 GI:15029483
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVERIN.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 213467)
REFERENCE
Waterston, R.H.
TITLE
The sequence of Homo sapiens clone
JOURNAL
Unpublished
AUTHORS
2 (bases 1 to 213467)
Waterston, R.H.
DIRECT SUBMISSION
Submitted (08-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jul 30, 2001 this sequence version replaced gi:14627163.

COMMENT
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Center project name: H.NH0480A06
----- Project Information -----
----- Summary Statistics -----
Sequencing vector: MJ3, 338
Sequencing vector: plasmid, 358
Chemistry: Dye-Primer ET; 338 of reads
Chemistry: Dye-terminator Big Dye; 358 of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 198028 bases at least Q40
Consensus quality: 200051 bases at least Q30
Consensus quality: 209092 bases at least Q20
Insert size: 192000; agarose-fp
Insert size: 211898; sum-of-contigs
Quality coverage: 7.79 in Q20 bases; sum-of-contigs
Quality coverage: 7.63 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
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* 769: contig of 769 bp in length
* 770
* 869: gap of unknown length
* 870
* 192693: contig of 191824 bp in length
* 192694
* 192793: gap of unknown length
* 192794
* 194176: contig of 1383 bp in length
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* 194276: gap of unknown length
* 194277
* 195666: contig of 1390 bp in length
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* 195766: gap of unknown length
* 195767
* 197524: contig of 1758 bp in length
* 197525
* 197624: gap of unknown length
* 197625
* 199334: contig of 1710 bp in length
* 199335
* 199434: gap of unknown length
* 199435
* 201995: contig of 2561 bp in length
* 201996
* 202095: gap of unknown length
* 202096
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* 203377
* 203476: gap of unknown length
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FEATURES
Source

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XX WPI: 1999-229535/19.
XX DR
XX P-Psdb; AAW98179.
XX
XX DNA encoding inhibitor of cyclin-dependent kinase
XX
XX Claim 1b; Page 72-74; 88bp; English.

CC This is the DNA sequence of FL39, a cDNA clone that encodes a new
CC cyclin-dependent kinase (CDK) inhibitor (see AAW98179) of Arabidopsis
CC thaliana. New plant products with a putative CDK inhibitory
CC function were screened by using a two-hybrid system with CDC2a2
CC protein as bait and a library made from an RNA mixture of A.
CC thaliana cell suspensions harvested at the early exponential,
CC exponential, early stationary and stationary phases. Positive
CC clones LDV39, LDV66 and LDV159 were obtained. Clone FL39 was
CC isolated from a flower cDNA library using partial clone LDV39 as
CC probe. Clone FL66 (see AAX25010) was similarly obtained using LDV66.
CC Another CDK inhibitor, AtPCD1 (see AAX25018), was obtained from
CC alfalfa. Results established that several CDK inhibitors exist
CC in plants and that these inhibitors are expressed at different
CC time points and may have different functions during the development
CC of the plant. CDK inhibitors, nucleic acids, antibodies, promoter
CC sequences, related recombinant DNA and vectors are all useful: for
CC diagnosis (no details); for modulating the cycle, division and/or
CC growth of plant cells; for altering activity of CDK; for modulating
CC growth inhibition in plants caused by environmental stress; for
CC inducing male or female sterility; for altering cell division
CC progression in plants, bacteria, fungi, insect and animal cells;
CC and to screen for agonists or antagonists that are potentially
CC useful as growth regulators or herbicides. Plants of any sort can
CC be treated, e.g. to alter their size or resistance to disease.

Sequence 932 BP; 289 A; 125 C; 254 G; 264 T; 0 other;

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DT	18-OCT-2000	(first entry)
XX		
DE	Arabidopsis thaliana	DNA fragment SEQ ID NO: 47486.
XX		
KW	Hybridisation assay; genetic mapping; gene expression control;	
KM	protein identification; signal transduction pathway;	
KW	metabolic pathway; promoter; termination sequence; ss.	
XX		
OS	Arabidopsis thaliana.	
XX		
PN	EP1033405-A2.	
XX		
PD	06-SEP-2000.	
XX		
PF	25-FEB-2000;	2000EP-0301439.
XX		
PR	25-FEB-1999;	99US-0121825.
PR	05-MAR-1999;	99US-0123180.
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PR 27-AUG-1999; 99US-0151080.
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PR 31-AUG-1999; 99US-0151438.
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PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
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PR 18-OCT-1999; 99US-0159584.

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PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
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Query Match 91.0%; Score 848.2; DB 21; Length 883;
Best Local Similarity 99.6%; Pred. No. 4,9e-185;

Matches 850; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 9 gagaacacaacacgacacatacgaatgattttagagagagatagagatcggaag 68
DB 31 gagaacacaacacgacacatacgaatgattttagagagagatagagatcggaag 90
OY 69 tgaagctcgttagagagatattgagcggttagagagagagagatgltgttgaagaga 128
DB 91 tgaagctcgttagagagatattgagcggttagagagagagagatgltgttgaagaga 150
OY 129 atggaatttcgagcagcagcgtgtaaacgagagatgtagagagagagatgtagt 188
DB 151 atggaatttcgagcagcagcgtgtaaacgagagatgtagagagagagatgtagt 210
OY 189 aatctagagatlaattctgtctcgtgtgtacagagcagacatcggttggatgtggcga 248
DB 211 aatctagagatlaattctgtctcgtgtgtacagagcagacatcggttggatgtggcga 270
OY 249 gaattcagaagagagcgtctggagagagatggttttagttagacagcgagatctccctc 308
DB 271 gaattcagaagagagcgtctggagagagatggttttagttagacagcgagatctccctc 330
OY 309 cggttgaagaacagtggttcaaatcgagaagaatctcgtgttctgttctacat 368
DB 331 cggttgaagaacagtggttcaaatcgagaagaatctcgtgttctgttctacat 390
OY 369 cggagaagagaatcgagaacgagagaatcgaattgttagaattcttgaggaataacagtgtagcg 428
DB 391 cggagaagagaatcgagaacgagagaatcgaattgttagaattcttgaggaataacagtgtagcg 450
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DB 451 atcgttaaacagagaacgtgtgtgatttagatgatttgaagaatgtagagatcgatga 510
OY 489 acatgagatctctctcgtgtgtgttgaagatgtagagatcgtccgcagaggttaaggaaga 548
DB 511 acatgagatctctctcgtgtgtgttgaagatgtagagatcgtccgcagaggttaaggaaga 570
OY 549 gttccatagaacggttgaagaagctgtagaagatcttttccaggtgcgaggaag 608
DB 571 gttccatagaacggttgaagaagctgtagaagatcttttccaggtgcgaggaag 630
OY 609 atcttcggaataagttgttggaaatgttctatgaagataacttcgaattcgaagaagtg 668
DB 631 atcttcggaataagttgttggaaatgttctatgaagataacttcgaattcgaagaagtg 690
OY 669 agccacttggtgaggaagatacgaagtggttaaatgaatcagaagaagacatgat 728
DB 691 agccacttggtgaggaagatacgaagtggttcaaatgaatccagaagaagacatgat 750
OY 729 gataatgatgataatgttctccaccaagtaacttatttcttctgttaataatctt 788

DB 751 gataatgatgataatgttctccaccaagtaacttatttcttctgttaataatctt 810
OY 789 gcttgaatttctttaaacaataatcgaatgagatattctctcgaataatcaata 848
DB 811 gcttgaatttctttaaacaataatcgaatgagatattctctcgaataatcaata 870
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DB 871 acatgtaattcaa 883
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AC AAC37798;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 18698.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway;
KM metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
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PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
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PR 06-APR-1999; 99US-0128234.
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PR 06-MAY-1999; 99US-0132486.
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PR 06-AUG-1999;	9905-0147303.	PR 28-OCT-1999;	9905-0161992.
PR 06-AUG-1999;	9905-0147416.	PR 29-OCT-1999;	9905-0162142.

Query Match

Best Local Similarity

Matches 853; Conservative

90.28; 99.68; 0;

Score 840.8; DB 21; Pred. No. 2.4e-183; Mismatches 2; Indels 1; Gaps 1;

[illegible]

KM	root cell; meristem; leaf; ss.
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OS	Arabidopsis thaliana.
XX	
FH	Key
FT	69..620
CDS	/tag= a
FT	/product= BRO3
XX	
PN	WO200069883-A1.
PD	23-NOV-2000.
XX	
PF	15-MAY-2000; 2000WO-US13379.
XX	
PR	14-MAY-1999; 99US-0134373.
XX	
PA	(HUTC-) HUTCHINSON CANCER RES CENT FRED.
XX	
PI	Roberts J, Kelly B;
DR	WPI; 2001-024998/03.
P-PSDB; AAB47004.	
XX	
PT	Functionally inactivating expression of plant D-like cyclin inhibitor gene for producing a hyperplastic variant plant, modulating the growth and/or yield of plants, and increasing the proportion of dividing cells
XX	
PS	Example 1; Page 39-40; 50pp; English.
XX	
CC	The sequence given in AAC85204 represents a plant D1 cyclin inhibitor gene, BRO3. This sequence was isolated using a yeast two hybrid screen. The BRO3 protein was found to contain a seven amino acid sequence cyclin binding domain similar to that of BRO1, BRO2 and BRO4 (See also AAB47005-6). This sequence is homologous to a sequence present in a D-like cyclin inhibitor gene and when integrated at the corresponding locus, functionally inactivates plant D-like cyclin inhibitor protein expression. The BRO4 coding sequence may be used to produce a hyperplastic variant plant, increase the growth rate of a plant, or increase the proportion of dividing cells in a plant cell population, relative to a wild-type plant, by functionally inactivating the expression of a plant D-like cyclin inhibitor gene in a plant. BRO4 is useful for increasing the proportion of dividing cells in a plant cell population comprising protoplast, seeds, root cells, meristem cells or leaf cells.
CC	
XX	
SQ	Sequence 809 BP; 268 A; 110 C; 213 G; 218 T; 0 other:
Query Match	80.7%; Score 751.8; DB 22; Length 809;
Best Local Similarity	99.7%; Pred. No. 5,4e-163;
Matches 753; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
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OY	169 gaggagaagtgaatttagtggaaactagaataattcttgttcctggtgtgtcacgacgaa 228
Db	74 ggaggaagtgaatttagtggaaactagaataattcttgttcctggtgtgtcacgacgaa 133
OY	229 tcgcggtgtaattgttggcgaagaattcaacagaagcttcggcgacacagtggttatagt 288
Db	134 tccggttgtaattgttggcgaagaattcaacagaagcgttcggagaacgagtggttatagt 193
OY	289 accaagcggaattccctcccggttgtaaacaagctgtccaatcgaaagaagaagtctgc 348
Db	194 acgaagcggaattccctcccggttgtaaacaagctgtccaatcgaaagaagaagtctgc 253
OY	349 ggttcogtgttcttaccatcgaaagaagaatcgaaacggaagaatgtttaagt 408
Db	254 ggttcogtgttcttaccatcgaaagaagaatcgaaacggaagaatgtttaagt 313

QY 409 tgaagaaataacgctgacgacatcgtaacagaacgctggaattacgatatgaa 468
 |||||||
 Db 314 tggagaaataacgctgacgacatcgtaacagaacgctggaattacgatatgaa 373
 |||||||
 QY 469 taagatgaggaatcgatgacatggaattctcttcggtgctgtgaagatgagtc 528
 |||||||
 Db 374 taagatgaggaatcgatgacatggaattctcttcggtgctgtgaagatgagtc 433
 |||||||
 QY 529 tgcgcgaaggttaaggaaggttccttcgaagcgtgaaggaagcgtgaaggttc 588
 |||||||
 Db 434 tgcgcgaaggttaaggaaggttccttcgaagcgtgaaggaagcgtgaaggttc 493
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 QY 589 ttctcaggtgctgaggaagaatcttcggaataagttgtgaagtctctgaagtaaa 648
 |||||||
 Db 494 ttctcaggtgctgaggaagaatcttcggaataagttgtgaagtctctgaagtaaa 553
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 QY 649 ctccgatttcgagaagaatgagccactgtgtgaggaagaagatgaggttaattgaa 708
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 Db 554 ctccgatttcgagaagaatgagccactgtgtgaggaagaagatgaggttaattgaa 613
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 QY 709 tccatgagaagaacgcatgatatgatatctgtttccaccagaagctattat 768
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 Db 614 tccatgagaagaacgcatgatatgatatctgtttccaccagaagctattat 673
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 QY 769 ttctctgtaataatcttgccttgaattttcttcaacaataccaagtatgata 828
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 Db 674 ttctctgtaataatcttgccttgaattttcttcaacaataccaagtatgata 733
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 QY 829 ttctctgtaataatcaataatgtaattcaact 863
 |||||||
 Db 734 ttctctgtaataatcaataatgtaattcaact 768
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 RESULT 5
 AA229416 standard; cDNA; 755 BP.
 ID AA229416:
 AC AA229416:
 XX
 DT 29-FEB-2000 (first entry)
 DE Arabidopsis thaliana CDK inhibitor, ICK2 encoding cDNA.
 XX
 XX Cyclin-Dependent Kinase Inhibitor; CDK; Interactor of Cdc2 Kinase 2;
 KM ICK2; Cdc2a; D-class cyclin; CYCD1; CYCD2; CYCD3; morphogenesis;
 KM antisense construct; tissue-specific promoter; transgenic plant;
 KM male sterility; ds.
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..531
 FT /product= "ICK2"
 FT
 XX
 PN MO9964599-A1.
 PD 16-DEC-1999.
 XX
 PE 08-JUN-1999; 99MO-CA00532.
 XX
 PR 08-JUN-1998; 98CA-2235978.
 PR 31-DEC-1998; 98CA-2256121.
 XX
 PA (MIAC) AGRIC & AGRIFOOD CANADA.
 PA (UTSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
 PA (CANADA) NAT RES COUNCIL CANADA.
 XX
 PI Mang H, Fowke LC, Crosby WL;
 DR WPI: 2000-097540/08.
 DR P-PSDB: AAY44336.
 XX

PT Modifying plant cell development using nucleic acid encoding inhibitor
 PT of cyclin-dependent kinase, or corresponding antisense sequence, e.g.
 PT for inducing male sterility -
 XX
 PS Disclosure; Fig 3; 58pp; English.
 XX
 CC The present sequence is a cDNA encoding ICK2 which inhibits A. thaliana
 CC Cyclin-Dependent Kinase (CDK). Interactor of Cdc2 Kinase 2 (ICK2)
 CC interacts with Cdc2a, D-class cyclins, CYCD1, CYCD2 and CYCD3 and
 CC shares functional and sequence similarity with ICK1. Growth,
 CC morphogenesis, multiplication, enlargement, differentiation and
 CC maturation of plant cells can be modified by transforming them with
 CC nucleic acid encoding CDK inhibitor or antisense construct complementary
 CC to the inhibitor gene, operably linked to a tissue-specific promoter.
 CC The transgenic plants exhibit alteration of traits such as petals, male
 CC sterility and ability to set seeds.
 XX
 SQ Sequence 755 BP; 229 A; 106 C; 187 G; 233 T; 0 other:

Query Match 79.9%; Score 744.8; DB 21; Length 755;
 Best Local Similarity 99.7%; Pred. NO. 2.1e-161;
 Matches 746; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 185 gtgaatctagaataatctgtctccgtgtgtacagcgacgaatcgcggtgatactg 244
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 Db 1 gtgaatctagaataatctgtctccgtgtgtacagcgacgaatcgcggtgatactg 60
 |||||||
 QY 245 gggagaattcagcagagcgctcggaagcagagtggtttatagtaacagcgagatct 304
 |||||||
 Db 61 gggagaattcagcagagcgctcggaagcagagtggtttatagtaacagcgagatct 120
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 QY 305 cctccggttgagaagacggtgtcacaatcgagaagaagacgtcgtgtctgtgtct 364
 |||||||
 Db 121 cctccggttgagaagacggtgtcacaatcgagaagaagacgtcgtgtctgtgtct 180
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 QY 365 acatcgaagaagaatcgaacacggaatcgaattctgtagaacctgaagaaataacggt 424
 |||||||
 Db 181 acatcgaagaagaatcgaacacggaatcgaattctgtagaacctgaagaaataacggt 240
 |||||||
 QY 425 gacgatcgtgaacacagaacgctgtgatttaacgatattgaataagatgagaatcg 484
 |||||||
 Db 241 gacgatcgtgaacacagaacgctgtgatttaacgatattgaataagatgagaatcg 300
 |||||||
 QY 485 atgacaatgaggtctcttcggtgctgtgaagatgagagtcgcgcgaggttaag 544
 |||||||
 Db 301 atgacaatgaggtctcttcggtgctgtgaagatgagagtcgcgcgaggttaag 360
 |||||||
 QY 545 aagatctcacaagcgtgaaggaagctgagttaagaagaatttttcaagtgcgag 604
 |||||||
 Db 361 aagatctcacaagcgtgaaggaagctgagttaagaagaatttttcaagtgcgag 420
 |||||||
 QY 605 aaagatctcggaataagtggtgaagtctatgaagttaacttgatttcgagaa 664
 |||||||
 Db 421 aaagatctcggaataagtggtgaagtctatgaagttaacttgatttcgagaa 480
 |||||||
 QY 665 gatagccaactgtgtgaggaagatagcagtggtttaatgaatccaatgagaagaga 724
 |||||||
 Db 481 gatagccaactgtgtgaggaagatagcagtggtttaatgaatccaatgagaagaga 540
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 QY 725 tgatgataatgatcatctgtttcaccaagaactattattttcttgataat 784
 |||||||
 Db 541 tgatgataatgatcatctgtttcaccaagaactattattttcttgataat 600
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 QY 785 ctggtctgtattttcttcaacaataccaatgtatatactttctcgaataatc 844
 |||||||
 Db 601 ctggtctgtattttcttcaacaataccaatgtatatactttctcgaataatc 660
 |||||||
 QY 845 aatacatgataatcaactttgttgaactccttgaggttaataatagatcggtt 904
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 Db 661 aatacatgataatcaactttgttgaactccttgaggttaataatagatcggtt 720
 |||||||
 QY 905 ttctcgattaaataactaagttat 932

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Db 721 ttctcgtatataactaataagtttat 748
RESULT 6
AAC36219
ID AAC36219 standard; DNA; 585 BP.
XX
AC AAC36219;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 12982.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW Protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
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PR 06-MAY-1999; 99US-0132486.
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PR 24-MAY-1999; 99US-0135629.
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PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
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PR 08-JUN-1999; 99US-0138094.
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PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
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PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.

PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
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PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
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PR 18-JUN-1999; 99US-0139463.
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PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
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PR 23-JUN-1999; 99US-0140353.
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PR 24-JUN-1999; 99US-0140695.
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PR 16-AUG-1999; 99US-0149368.

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PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
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PR 21-OCT-1999; 99US-0160815.
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PR 22-OCT-1999; 99US-0160989.
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PR 25-OCT-1999; 99US-0161405.
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PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161320.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.
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Query Match 23.9%; Score 223; DB 21; Length 585;

Best Local Similarity 95.6%; Pred. No. 5e-42;

Matches 240; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

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QY 610 tcttcggaataagttgtaagttctatgaagtaacttcgatttcgagaagaatga 669
DB 335 tcaaggaataatgaagttgtaagttctatgaagtaacttcgatttcgagaagaatga 394
QY 670 gcaacttggtgaggaagaacagagtggttaaatgaatcgaatgaagaagacgatgatg 729
DB 395 gcaacttggtgaggaagaacagagtggttaaatgaatcgaatgaagaagacgatgatg 454
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QY 730 ataatagtacatctgtttccaccaagaactactatactttctctcgtataatcttg 789
DB 455 ataatagtacatctgtttccaccaagaactactatactttctctcgtataatcttg 514
QY 790 ctttgatcttcttttaacaaatccaaatgtagatacttctctcgtaatatc-aata 848
DB 515 ctttgatcttcttttaacaaatccaaatgtagatacttctctcgtaatatc-aata 574
QY 849 acatgtaattc 859
DB 575 acatgtaattc 585
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RESULT 7

AAF58252/c

ID AAF58252 standard; DNA; 936 BP.

AAF58252;

24-APR-2001 (first entry)

Oligonucleotide D1835.

Electron-transfer group; ETM; mismatch; genotyping;

gene expression; ss.

Synthetic.

WO200107665-A2.

26-JUL-2000; 2000MO-US20476.

26-JUL-1999; 99US-0145695.

17-MAR-2000; 2000US-0190259.

(CLIN-) CLINICAL MICRO SENSORS INC.

Umeck RM;

WPI; 2001-159728/16.

Nucleic acids containing electron-transfer group, useful as labels in

hybridization assays, e.g. for genotyping, allowing repeat analyses on

a single surface

Example 6; Page 127; 159pp; English.

The present invention relates to a composition comprising two nucleic

acids each containing an electron-transfer group (ETM) having

different redox potentials. The invention is used for electronic

detection of nucleic acids, especially of substitutions (mismatches)

and single-nucleotide polymorphisms, e.g. for genotyping,

monitoring gene expression.

Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;

Query Match 12.5%; Score 116.8; DB 22; Length 936;

Best Local Similarity 6.3%; Pred. No. 1.1e-17;

Matches 55; Conservative 455; Mismatches 356; Indels 0; Gaps 0;

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QY 63 gaaagtgacgtcgttagagatatagcgcggttaggaagaagaacgagatggttg 122
DB 905 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 846
QY 123 aaggaatggaatgaacgaacgaacgagtgtaacgaagaagatgagaggaatgatt 182
DB 845 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 786
QY 183 tagtgaatcgaagataatctctcgcgtgtgtacagggcgaacgcggtggaattg 242
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```
QY 123 aagagaatgagttacgacgacggtgaaacgaagaatgaggaatgagtt 182
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 845 GCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 786
QY 183 tagtgaatctagataatctgtctccgtgtgtacagcgacgaatcggtgaattg 242
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 785 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 726
QY 243 tggcgaagaattcagcagcgctcgagacgaagtgtgtatctgacgacgagatt 302
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 725 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 666
QY 303 ctctccggttgaaagacagtgtaaatcgaagaagaattcgctgttcgtgtgt 362
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 665 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 606
QY 363 ctacatcggaagagaatcgaacgagaaatcgaaatctgtagatcttgagaaataacg 422
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 605 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 546
QY 423 gtgacgactgtgaacgaaacgctcggtgattcagatgttgaataagaatgagaaat 482
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 545 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 486
QY 483 cgatgaacatgatactctctcgtgtgtgtgaagatgtagtctcgcgcaggttaa 542
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 485 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 426
QY 543 ggaagagcttcacgagacggtgaaagacgtgagtagaagaatttttcaagtgcgcg 602
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 425 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 366
QY 603 agaaagatctcggaataagttgtgtgaatgtctatgaataactcgattcgaga 662
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 365 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 306
QY 663 aagatgagccactgtgtgaggaagatacgatggttaattgaatccatgaagaagac 722
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Db 305 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 246
QY 723 gatgataataatgataatgtttcaaccgaactataatcttctctgtaata 782
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 245 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 186
QY 783 atcttctctgattcttctcttcaacaatccaatgtagatctctctcogaataa 842
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Db 185 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 126
QY 843 tcaataacatgtaactcaacttctgtgtactccttgagtaataatagattcgtg 902
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Db 125 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 66
QY 903 tttctcgaataaataaataaattat 932
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Db 65 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 36

RESULT 12
AAF58255/c
ID AAF58255 standard; DNA; 938 BP.
XX
XX AAF58255;
AC
XX
XX 24-APR-2001 (first entry)
DE
XX oligonucleotide D1876.
KW
XX Electron-transfer group; ETM; mismatch; genotyping;
KV gene expression; ss.
XX
XX Synthetic.
OS
XX
XX WO200107665-A2.
PN
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XX
XX 01-FEB-2001.
PD
XX
XX 26-JUL-2000; 2000WO-US20476.
PF
XX
XX 26-JUL-1999; 99US-0145695.
PR 17-MAR-2000; 2000US-0190259.
XX
XX (CLIN-) CLINICAL MICRO SENSORS INC.
PA
XX
XX Dmek RM;
PI
XX
XX WPI; 2001-159728/16.
XX
XX Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface
XX
XX Example 6; Page 127; 159pp; English.
XX
XX The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
XX Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;
XX
XX
XX Query Match 12.5%; Score 116.8; DB 22; Length 938;
XX Best Local Similarity 6.3%; Pred. No. 1.1e-17;
XX Matches 55; Conservative 459; Mismatches 356; Indels 0; Gaps 0;
QY 63 ggaagtgactcgttagaataatgagcggttagagaagaagaatgagttg 122
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 905 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 846
QY 123 aagagaatgagttacgacgacggtgaaacgaagaatgaggaatgagttgatt 182
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 845 GCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 786
QY 183 tagtgaatctagataatctgtctccgtgtgtacagcgacgaatcggtgaattg 242
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 785 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 726
QY 243 tggcgaagaattcagcagcgctcgagacgaagtgtgtatagatacagcgagatt 302
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 725 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 666
QY 303 ctctccggttgaaagacagtgtaaatcgaagaagaatcggttcgtgtgtt 362
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 665 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 606
QY 603 ctacatcggaagagaatcgaacgagaaatcgaaatctgtagatcttgagaaataacg 422
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 605 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 546
QY 423 gtgacgactgtgaacgaaacgctcggtgattcagatgttgaataagaatgagaaat 482
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 545 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 486
QY 483 cgatgaacatgatactctctcgtgtgtgtgaagatgtagtctcgcgcaggttaa 542
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 485 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 426
QY 543 ggaagagcttcacgagacggtgaaagacgtgagtagaagaatttttcaagtgcgcg 602
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 425 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 366
QY 603 agaaagatctcggaataagttgtgtgaatgtctatgaataactcgattcgaga 662
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 365 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 306
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```
XX Nucleic acids containing electron-transfer group, useful as labels in
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PT a single surface
XX
XX Example 6; Page 127; 159pp; English.
XX
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CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
XX Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;
SQ

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Best Local Similarity 1.0%; Pred. No. 2,4e-16;
Matches 6; Conservative 395; Mismatches 220; Indels 0; Gaps 0;

QY 312 ttgaagaacagtgccaatcgagaagaagatcggtcggttctgttctacatcg 371
DB 132 www. ....
QY 372 aagagaatcgaaacgaggaatcgatttgatcttgaggaataacggtgacgac 431
DB 192 www. ....
QY 432 gtgaacagaacgctggaatcgatgaatgtgaataagaagtcgacgaac 491
DB 251 www. ....
QY 491 tgcaggaacggtgaagaagctgagtagaagatttttcaggtgcgagaagaatc 611
DB 372 www. ....
QY 612 ttcggaataagtgctggaatgctcgaataactcgattcgagaagaatgagc 671
DB 432 www. ....
QY 671 cactgtgtgaggaagatcgagtggttaaatcgaaacctgaagaagacgatgat 731
DB 492 www. ....
QY 732 aatgatacatgttttcaccaaagtaactataattttctcgtataatcttgct 791
DB 552 www. ....
QY 792 ttgatttcttcaacaataccaatgtagatacttctcgcgaataacaataca 851
DB 612 www. ....
QY 852 tgaatacaactttgttgtaactcctcgtgaggaataataatagatcgttttccgc 911
DB 672 www. ....
QY 912 ataataaactaagttat 932
DB 732 www. ....

RESULT 15
AAF58257
ID AAF58257 standard; DNA; 936 BP.
XX
AC AAF58257;
XX
DT 24-APR-2001 (first entry)
```

```
XX Oligonucleotide D1954.
DE
XX Electron-transfer group; ETM; mismatch; genotyping;
XX gene expression; ss.
XX
XX Synthetic.
XX
XX WO200107665-A2.
XX
XX 01-FEB-2001.
XX
XX 26-JUL-2000; 2000WO-US20476.
XX
XX 26-JUL-1999; 99US-0145695.
XX
XX 17-MAR-2000; 2000US-0190259.
XX
XX (CLIN-) CLINICAL MICRO SENSORS INC.
XX
XX Unk RM;
XX
XX WPI: 2001-159728/16.
XX
XX Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
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XX
XX Example 6; Page 127; 159pp; English.
XX
CC The present invention relates to a composition comprising two nucleic
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CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
XX Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;
SQ

Query Match 11.9%; Score 111; DB 22; Length 936;
Best Local Similarity 1.0%; Pred. No. 2,4e-16;
Matches 6; Conservative 395; Mismatches 220; Indels 0; Gaps 0;

QY 312 ttgaagaacagtgccaatcgagaagaagatcggtcggttctgttctacatcg 371
DB 132 www. ....
QY 372 aagagaatcgaaacgaggaatcgatttgatagcttgaggaataacggtgacgac 431
DB 192 www. ....
QY 432 gtgaacagaacgctggaatcgatgaatgtgaataagaagtcgacgaac 491
DB 252 www. ....
QY 492 tgcaggaacggtgaagaagctgagtagaagatttttcaggtgcgagaagaatc 611
DB 312 www. ....
QY 612 ttcggaataagtgctggaatgctcgaataactcgattcgagaagaatgagc 671
DB 432 www. ....
QY 671 cactgtgtgaggaagatcgagtggttaaatgcaatcgaaagaacgatgat 731
DB 492 www. ....
QY 732 aatgatacatgttttcaccaaagtaactataattttctcgtataatcttgct 791
DB 551 www. ....
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[illegible]

Search completed: January 30, 2002, 11:56:16
Job time: 2855 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 30, 2002, 11:04:46 ; Search time 1206.98 Seconds
(without alignments)
8297.624 Million cell updates/sec

Title: US-09-574-735C-1
Sequence: 1 ggcacggagggaaccacacaa.....ttaataactataagtttat 932

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues
Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estipl:*
6: em_estlba:*
7: em_estro:*
8: em_estov:*
9: em_hlc:*
10: gb_estl:*
11: gb_estl2:*
12: gb_hlc:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_hiv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rod:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
c 1	69.6	7.5	1101 13	CNS0039G	AL063921 Drosophila
c 2	58.4	6.3	928 13	CNS00DKY	AL071865 Drosophila
c 3	57.2	6.1	1101 13	CNS00DEVL	AL069706 Drosophila
c 4	56	6.0	997 13	CNS005TE	AL060767 Drosophila
c 5	55.6	6.0	1092 13	CNS020K7	AL175666 Tetradon
c 6	54.6	5.9	1101 13	CNS0039G	AL063921 Drosophila
c 7	54	5.8	702 11	BF863173	BF863173 963041R12
c 8	53.8	5.8	1101 13	CNS000T2	AL078714 Drosophila
c 9	53.4	5.7	1101 13	CNS017V2	AL108536 Drosophila
c 10	52.8	5.7	1101 13	CNS00293	AL109737 Drosophila
c 11	52.6	5.6	1225 13	CNS0161D	AL106171 Drosophila
c 12	52	5.6	1101 13	CNS017KX	AL108171 Drosophila

Result No.	Score	Query Match	Length DB	ID	Description
c 13	51.8	5.6	1201 13	CNS0163J	AL106249 Drosophila
c 14	51.4	5.5	1101 13	CNS00LJT	AL068307 Drosophila
c 15	51.2	5.5	970 13	CNS0182E	AL108800 Drosophila
c 16	50.6	5.4	1101 13	CNS00LJM	AL068473 Drosophila
c 17	50.4	5.4	467 13	CNS018G8	AL109288 Drosophila
c 18	50.4	5.4	996 13	CNS00DFUH	AL1071063 Drosophila
c 19	50	5.4	524 13	CNS01090	AL167541 Tetradon
c 20	49.8	5.3	1101 13	CNS00DEJ4	AL069257 Drosophila
c 21	49.6	5.3	889 13	CNS006MT	AL065765 Drosophila
c 22	49.6	5.3	1083 13	CNS001H6	AL074775 Drosophila
c 23	49.4	5.3	1086 13	CNS000YXK	AL096962 Drosophila
c 24	49.4	5.3	1101 13	CNS001FB	AL060732 Drosophila
c 25	49.2	5.3	1094 13	CNS012FZ	AL101513 Drosophila
c 26	49.2	5.3	1101 13	CNS000D1	AL065414 Drosophila
c 27	49	5.3	1002 13	CNS001XA	AL075355 Drosophila
c 28	48.8	5.2	697 13	A2124243	A2124243 T223107b
c 29	48.8	5.2	707 13	A2124244	A2124244 T223108b
c 30	48.8	5.2	1101 13	CNS00DFU	AL071076 Drosophila
c 31	48.8	5.2	3939 13	BH001059	BH001059 T122513b
c 32	48.6	5.2	1101 13	CNS016L1	AL106896 Drosophila
c 33	48.6	5.2	1101 13	CNS017KE	AL108152 Drosophila
c 34	48.4	5.2	876 13	CNS0009G1	AL053529 Drosophila
c 35	48.4	5.2	887 13	A2544590	A2544590 ENTDE54TR
c 36	48.4	5.2	1063 13	CNS07A2Y	AL436064 T3 end of
c 37	48.2	5.2	607 13	BH004535	BH004535 BMBAG08B2
c 38	48.2	5.2	906 13	A2527585	A2527585 ENTCE20TR
c 39	48.2	5.2	908 13	BH131383	BH131383 ENTND36TF
c 40	48.2	5.2	987 13	CNS00418	AL066537 Drosophila
c 41	48.2	5.2	1092 13	CNS020K7	AL175666 Tetradon
c 42	48.2	5.2	1101 13	CNS0026Z	AL1097301 Drosophila
c 43	48	5.2	848 13	A2689328	A2689328 ENTHF58TF
c 44	48	5.2	905 13	CNS000KH	AL077798 Drosophila
c 45	48	5.2	1001 13	CNS0155H	AL105023 Drosophila

ALIGNMENTS

RESULT 1
CNS0039G/c
LOCUS
DEFINITION
CNS0039G 1101 bp DNA
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AL063921
AL063921.1 GI:4941778
GSS.
fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)

REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)

COMMENT
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammosser in Pletier de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
source

Location/Qualifiers
1. .1101
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BAC08K10"
/note="end : PCR3"

BASE COUNT 201 a 64 c 131 g 202 t 503 others
ORIGIN

Query Match 7.5% Score 69.6; DB 13; Length 1101;
Best Local Similarity 18.0%; Pred. No. 0.00079;
Matches 108; Conservative 245; Mismatches 247; Indels 0; Gaps 0;

OY 310 ggttgaagaacagctgcaatcgaagaagaagattcgtggttctgttctacac 369
DB 997 RGAGKRRDRADATDAGAGRRGRRKKRDKDGDGDKKKKAKAKAAKATKMD 938
OY 370 ggaagagaatcgaaacgagaaatcgatttgaatttggagaataacggtgag 429
DB 937 WMDKDKMKWGADRRKADDDGAGDDGKADDDTGTGDDDKDKMDWDKAKGT 878
OY 430 tctggaacgaacgctgctgagattcagatgattgaataagagtagaatacga 489
DB 877 WGDATMAAATDMMWGMADADMTWDAADDMWADDRMDAMKMDAMWGAFTADR 818
OY 490 catgattcttctcgtgctgctgagatgtagctcgccgaggttaagaagag 549
DB 817 DWGDRAGKRGAGRRRRKRRADDRADDDAATWTTTDTTDDMKDRKARRRRRT 758
OY 550 tctccatgagacggtgagaaagctgagtagaagatttctcaggtcggaaga 609
DB 757 WAADRTWDRDDDDRDADGAGTAAKRRKRRKRRKRRDADDDTADDRRRGDD 658
OY 610 tcttcggaataagctgtgagaaatgctatgaaatgaactcgattcgaagaatga 669
DB 697 ADACKGKKTKRRRRRRATWRTDAMWADAMWTTTDTDDMKDRKARRRRRT 638
OY 670 gccactgtgaggaagaatcagagtggttaactgaatccatgaagaagacga 729
DB 637 TARAAWMMWTKAMWAKWMMKRRADRWADTWDADRRKARDWAKAMWARRRR 578
OY 730 ataattgagctgtgttccaccaagtaactatttcttctcgtatatactctg 789
DB 577 AARDDRMTTKGKTITATWTTWAAKAAWMAWMAATITATWTTTWTWTTT 518
OY 790 cttgatttcttcttaacaacaatccaatgtagatacttctclogaataacata 849
DB 517 WTTTAAMWMAWMTATWAAWTAAMWMAAATTTTWTWTTTWTWMAWMTAWT 458
OY 850 catgataatcaacttctgttctactccttgaggttaataatagattcgtgtt 909
DB 457 WTTTWTWTTWMAATTTTWTWTTWMAATTAATTTTWTWTAATAAAMWMTWTAT 398

RESULT 2
CNS00DKY/c 928 bp DNA GSS 04-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC #
DEFINITION BACR27A24 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL071865
VERSION AL071865.1 GI:4948170
KEYWORDS
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 928)
Genoscope.
TITLE Direct Submission

JOURNAL

COMMENT

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
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please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazuhiro Osoegawa and
Aaron Mammosier in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
source

Location/Qualifiers
1. .928
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR27A24"
/note="end : T7"

BASE COUNT 262 a 70 c 84 g 321 t 191 others
ORIGIN

Query Match 6.3% Score 58.4; DB 13; Length 928;
Best Local Similarity 31.9%; Pred. No. 0.11;
Matches 72; Conservative 67; Mismatches 87; Indels 0; Gaps 0;

OY 701 aaatgaatccatgaaagacgatgataatgatcatcgtttccacaagaatgac 760
DB 865 ABAAMWTTTMAAAMAMAMCVMAMMMAMMMAMMTTMMNNHHNNHHNTTTT 806
OY 761 ttatatttcttctgtaataatctgttgaatttcttcttaacaataatcgaatg 820
DB 805 TTTTWTWTTTWTWTTTWTWTTTWTWTTTWTWTTTNNNNNCCHVAMATW 746
OY 821 tagatacttctcgaataatcaatcagtaactgaacttctgttctactcct 880
DB 745 WMMWTAATTTTATWMTWMAWMAAAMMAAAMMAAATTTTWTWTTTATTTT 686
OY 881 gaggaataatgaatcgttcttctcgaataataataacataa 926
DB 685 AATTTTATTTTWTWTTTWTWTTTWTATATTAAMATWAMANA 640

RESULT 3
CNS00EVL/c 1101 bp DNA GSS 04-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC:
DEFINITION BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL069706
VERSION AL069706.1 GI:4949849
KEYWORDS
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 1101)
Genoscope.
TITLE Direct Submission

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FEATURES

Location/Qualifiers

1..1101
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_1lb="RPCI-98"
/clone="BACR29B23"
/note="end : T7"
BASE COUNT 419 a 91 c 60 g 299 t 232 others
ORIGIN

Query Match 6.1%; Score 57.2; DB 13; Length 1101;
Best Local Similarity 38.0%; Pred. No. 0.18;
Matches 89; Conservative 46; Mismatches 99; Indels 0; Gaps 0;

QY 699 ttaaatgaatcgaagaagacgataatgataatgataatgattgtttaccacaagt 758
Db 1003 TWTAMTAAATATATATATAAATATATATAAATATAAATATAAATAA 944
QY 759 acctatattcttcgtaataatcttcgttattcttccttaacaataccaa 818
Db 943 TATTAAT 884
QY 819 tctgataatcttcctgaataatcaataatgaatcaatcttcgttattcc 878
Db 883 TWTATTTTAT 824
QY 879 ttgaggaatcaatgattcggtttcttcgataataataaattat 932
Db 823 WTTTAT 770

RESULT 4

CNS005TE/c 997 bp DNA GSS 03-JUN-1999
LOCUS
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR12K22 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION A1060767
VERSION
KEYWORDS
SOURCE
ORGANISM

fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 997)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequenage :
BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org>. The BDGP Drosophila melanogaster BAC library was prepared by Kazuoto Osoegawa and Aaron Mammeter in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial

EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

Location/Qualifiers

1..997
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_1lb="RPCI-98"
/clone="BACR12K22"
/note="end : TET3"
BASE COUNT 89 a 99 c 13 g 258 t 538 others
ORIGIN

Query Match 6.0%; Score 56; DB 13; Length 997;
Best Local Similarity 18.8%; Pred. No. 0.31; Mismatches 264; Indels 1; Gaps 1;
Matches 104; Conservative 185; Mismatches 264; Indels 1; Gaps 1;

QY 78 agagattatgcygcygtagagaaagaaagagatggttgtaagaatgagta 137
Db 997 ARARRRAGARARARRRRCRGARARARRRARRRARRRARRRARRRARRR 938
QY 138 cgaagcagcagtgaaacgaagatgagaggaagtgatttagtgatctaga 197
Db 937 AGARAAARARRRRARRRRARRRRARRRRARRRRARRRRARRRRARRRR 878
QY 198 taattcttcctcggtgtacagcgcaatcgcgcgtggaattgtgcgaatactc 257
Db 877 ARRRARAAARARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 818
QY 258 caggaagcgcggaagacggtgtgttagtaglacagcgcggaatctcctcgttgaa 317
Db 817 ARARARRRARRRARRRARRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 758
QY 318 aacggtccaatcgaagaagaatcgtcgttggtgtgtctcaccggaaga 377
Db 757 RARARAGARAAARRRRARRRARRRRRRRRRRRRRRRRRRRRRRRRRR 698
QY 378 aatcgaacggaagatcga-attgtagatcttgaggaataacggtgacatcgtga 436
Db 697 ARRRRRRGARARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 638
QY 437 acagaacgctcgtgattacgattgataaagatggaatcgaatcgaatcga 496
Db 637 RGARRRRRGARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 578
QY 497 tctctcgtggtggtggaagatgtagtctgcgcgagtgtaagaagatcctcat 556
Db 577 RRR 518
QY 557 gagaagcgaagcgaagcgaatgtaagaatttttcagtggtgcggaagaatcctcg 616
Db 517 RRRRRRRRGARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 458
QY 617 aataagtggtcga 630
Db 457 NNNNNNNNNNNNA 444

RESULT 5

CNS020K7/c 1092 bp DNA GSS 12-MAY-2000
LOCUS
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 22211 of library G from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION A1175696
VERSION A1175696.1 GI:7813753
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis

[illegible][illegible]

AUTHORS	Grossman, A., Davies, J., Federspiel, N., Harris, E., Hauser, C., Lefebvre, P., McDermott, J. P., Shrago, J., Silfow, C. and Stern, D.
TITLE	Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants; project phase 3
JOURNAL	Unpublished (2000)
COMMENT	Contact: Charles Hauser DCMB Box 91000 Duke University Durham, NC 27708-1000 Tel: 919 613 8159 Fax: 919 613 8177 Email: chauser@duke.edu. Location/Qualifiers
FEATURES	Source
source	1..702 /organism="Chlamydomonas reinhardtii" /strain="CC-1690 wild type mt+ 21gr" /db_xref="taxon:3055" /clone_lhb="C. reinhardtii CC-1690, stress condition I, normalized, lambda zap II" /note=Vector: Bluescript II SK-; Site_1: EcoRI; Site_2: XhoI; This library, constructed by John Davies and Jeffrey McMerrott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP-N (30 min, 1hr, 4hr), TAP-S (30 min, 1hr, 4hr), TAP-P (4hr, 12hr, 24hr), NO3 to NH4 (30min, 1hr , 4hr) and NH4 to NO3 (30min, 1hr, 4hr). PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda zap II (Stratagene) in the EcoRI (5') and XhoI (3') sites. Bluescript II SK- plasmids were excised from the lambda zap clones by superinfection with Exassist (Stratagene) phage. The library was normalized using method 4 described in Bonaldi et al (1996) Genome Research 6: 791-806."
BASE-COUNT	193 a 103 c 136 g 270 t
ORIGIN	
Query Match	5.8%; Score 54; DB 11; Length 702;
Best Local Similarity	57.4%; Pred. No. 0.79;
Matches 117; Conservative	0; Mismatches 85; Indels 2; Gaps 1;
OY	731 taatgatgatacatctgtttccaccaaagtactatttcttcctcgacaatccttgcc 790
Db	463 TAAATAAAATATATTATTTTAAATTAATGTTATTTATTTATTTATTTTATTTTAA 522
OY	791 ttgtatttctcttaacaaatccaatgtatgatat--cttctcctcgaaatacata 848
Db	523 TTTCATTTTTTAGTTTAAAAATTTTATATATATTTATTTATTTAAATTTTAAA 582
OY	849 acatgtaatcaactttgttgttacctccttgaggtaattaataatagaatcggttttc 908
Db	583 ATAGATAAATGAATTTTCATTATTTATTAATAAGAATATTAATTCACGTATTTTGG 642
OY	909 tcgattaataacataaagtttat 932
Db	643 ACTATATTTTACTATTAAGATAAT 666
RESULT	8
CNS00LT2	CNS00LT2 1101 bp DNA GSS 14-JUN-1999
LOCUS	Drosophila melanogaster genome survey sequence TRETS end of BAC:
DEFINITION	BACR4BP19 of RPCI-98 library from Drosophila melanogaster (fruit fly); genomic survey sequence.
ACCESSION	AL078714 GI:5102004
VERSION	GSS.
KEYWORDS	fruit fly.
SOURCE	Drosophila melanogaster
ORGANISM	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE	1 (bases 1 to 1101)

[illegible]

Best Local Similarity 39.6%; Pred. No. 1.9;
Matches 101; Conservative 35; Mismatches 119; Indels 0; Gaps 0;

QY 677 gctgaggaagaatagatggttaattgatacgaagaagacgataatga 736
DB 965 GGGGGGMMMMANNGGGGGGGAGGGKTNAAAAAATTTTAAATTTTWTW 906
QY 737 tgaatcgtttccacaagaactattatcttcttcgtataatccttgat 796
DB 905 MAMMMWMTAAATTAATTTTWTMAAAATATATKKTWAMWMAAMWTWAKTATTTTAAAT 846
QY 797 ttctcttaacaaatccaatgtagatatcttctcgaataataacatga 856
DB 845 TTTTWTWAKTAAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTA 786
QY 857 ttcaactttgttgaactccttgaggaataatagatcgttttctcgat 916
DB 785 ATTGAAGTATATGAKTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTA 726
QY 917 taaactaaagtta 931
DB 725 AAAAATATAATTTA 711

RESULT 14
CNS00LJT/c 1101 bp DNA GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC:
DEFINITION BACR30P10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL068307.1 GI:4958538
VERSION AL068307.1
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
Genoscope.
AUTHORS Direct Submission
TITLE Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT - Web : www.genoscope.cns.fr
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammosser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
source location/Qualifiers
1..1101
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_id="RPCI-98"
/clone="BACR30P10"
/note="end : T7"

BASE COUNT 507 a 148 c 112 g 171 t 163 others
ORIGIN

Query Match 5.5%; Score 51.4; DB 13; Length 1101;
Best Local Similarity 45.7%; Pred. No. 2.3;
Matches 79; Conservative 24; Mismatches 70; Indels 0; Gaps 0;

QY 742 atgtttccaccaagactattatttcttctcgtataatccttgattttc 801
DB 359 TTTTWTWAKTAAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 300

QY 802 tttaacaaatccaatgtagatatcttctcgaataataacatgaatca 861
DB 299 TTTTCMAAGTTTCTTGTATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 240

QY 862 cttctgttgaactccttgaggaataatagatcgttttctcgat 914
DB 239 TTTTGTCTTWTWTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 187

RESULT 15
CNS0182E 970 bp DNA GSS 26-JUL-1999
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC:
DEFINITION BACN37A19 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL108800.1 GI:5629104
VERSION AL108800
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Plasmid Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 970)
Genoscope.
AUTHORS Direct Submission
TITLE Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage:
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT - Web : www.genoscope.cns.fr
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
<http://www.edgp.ebi.ac.uk> - This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelOBAC11.

FEATURES
source location/Qualifiers
1..970
/organism="Drosophila melanogaster"
/plasmid="pBelOBAC11"
/db_xref="taxon:7227"
/clone_id="DrosBAC"
/clone="BACN37A19"
/note="end : T7"

BASE COUNT 214 a 147 c 153 g 315 t 141 others
ORIGIN

Query Match 5.5%; Score 51.2; DB 13; Length 970;
Best Local Similarity 35.6%; Pred. No. 2.6;
Matches 72; Conservative 48; Mismatches 82; Indels 0; Gaps 0;

QY 725 tgaatgaatgatacatgttttccacaagaactattatttcttctgataat 784
DB 766 TTTTAAATTAATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTA 825
QY 785 ctgttgatttatttcttcaacaaatccaaatgtagatatccttctcgaataac 844
DB 826 AMTMMWMTTWTWTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 885
QY 845 aatacatgtaatacactttgttgccttctcgaataataatagattcgt 904
DB 886 AATAAATWMTWATTAATGATWMTWTTTCTTCTTCTTCTTCTTCTTCTTCTT 945
QY 905 ttctcgatataataactaa 926
DB 946 AAAAAMWTTTAAAMWMAAAA 967

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 30, 2002, 11:07:41 ; Search time 45.26 seconds
(without alignments)
4665.665 Million cell updates/sec

Title: US-09-574-735C-1

Sequence: 1 ggcacggaggagaccacaa.....ttaataactaatttat 932

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued_Patents_NA:*

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- 2: /cgn2_6/prodata/2/lna/5B_COMB.seq:*
- 3: /cgn2_6/prodata/2/lna/6A_COMB.seq:*
- 4: /cgn2_6/prodata/2/lna/6B_COMB.seq:*
- 5: /cgn2_6/prodata/2/lna/PCOTUS_COMB.seq:*
- 6: /cgn2_6/prodata/2/lna/backfilesl.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	76.2	8.2	7218	1	US-08-232-463-14
c 2	49	5.3	51952	3	US-08-947-823-1
c 3	44.4	4.8	19124	2	US-08-487-825B-13
c 4	44	4.7	1689	1	US-07-991-867B-41
c 5	44	4.7	1689	2	US-08-544-332-41
c 6	44	4.7	8457	1	US-07-991-867B-1
c 7	44	4.7	8457	2	US-08-544-332-1
c 8	41.8	4.5	471	4	US-09-385-982-58
c 9	41.6	4.5	4090	4	US-08-569-214-4
c 10	41.6	4.5	4090	4	US-08-937-236-4
c 11	40.2	4.3	837	4	US-08-998-416-288
c 12	38.6	4.1	6243	2	US-09-056-075-1
c 13	38.2	4.1	1113	1	US-08-231-342-5
c 14	37.8	4.1	12124	1	US-08-181-315A-36
c 15	37.8	4.1	12124	1	US-08-449-315-36
c 16	37.8	4.1	12124	1	US-08-444-803-36
c 17	37.8	4.1	12124	1	US-08-449-043-36
c 18	37.8	4.1	12124	1	US-08-456-265A-36
c 19	37.8	4.1	12124	1	US-08-455-416-36
c 20	37.8	4.1	12124	1	US-08-455-244-36
c 21	37.8	4.1	12124	1	US-08-454-876-36
c 22	37.8	4.1	12124	2	US-08-457-364-36
c 23	37.8	4.1	12124	2	US-08-456-262-36
c 24	37.8	4.1	12124	2	US-08-456-240-36
c 25	37.8	4.1	12124	2	US-08-455-736-36
c 26	37.8	4.1	12124	2	US-08-971-217-36
c 27	37.8	4.1	12124	4	US-09-350-600-36

28	37.6	4.0	615	4	US-08-998-416-186	Sequence 186, App
c 29	37.4	4.0	2781	3	US-08-749-522-4	Sequence 4, App11
c 30	37.2	4.0	5852	1	US-07-867-106-2	Sequence 2, App11
c 31	37	4.0	1690	4	US-08-943-731-166	Sequence 166, App
c 32	37	4.0	17606	4	US-08-943-731-166	Sequence 4, App11
c 33	36.8	3.9	636	4	US-08-998-416-1137	Sequence 1137, App
c 34	36.4	3.9	19124	2	US-08-487-825B-13	Sequence 13, App11
c 35	36.2	3.9	734	3	US-09-014-583-1	Sequence 1, App11
c 36	36.2	3.9	1667	1	US-08-485-284A-1	Sequence 1, App11
c 37	36.2	3.9	6768	1	US-08-107-755A-1	Sequence 1, App11
c 38	36.2	3.9	8457	1	US-07-991-867B-1	Sequence 1, App11
c 39	36.2	3.9	8457	2	US-08-544-332-1	Sequence 1, App11
c 40	36	3.9	6216	3	US-09-213-053-1	Sequence 1, App11
c 41	36	3.9	8920	2	US-08-446-855A-1	Sequence 1, App11
c 42	36	3.9	8920	4	US-09-150-741-1	Sequence 1, App11
c 43	35.8	3.8	319	1	US-07-593-657-14	Sequence 14, App1
c 44	35.8	3.8	3095	6	5231168-1	Patent No. 5231168
c 45	35.6	3.8	872	4	US-08-998-416-487	Sequence 487, App

ALIGNMENTS

RESULT 1
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; City: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICANT APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935, 313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZ9pl-F1s
; US-08-232-463-14

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Query Match      8.2%; Score 76.2; DB 1; Length 7218;
Best Local Similarity 6.5%; Pred.No.4,6e-10;
Matches 27; Conservative 235; Mismatches 133; Indels 0; Gaps 0

Oy 43 ttgagagagatgaagatctggaagtgcgtctgtagagattaigcgcggttagag 102
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Db 1399 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1340

Oy 163 gatgcgaggaagtctatgttgaatctagaatactctgtctcgttgcacagc 222
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1339 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1280

Oy 223 gacgaatcggtgtgaattctgtgcgagaatcgcagagagcgtcgcgagagtg 282
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Db 1279 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1220

Oy 283 tatgtctcgcgcgcgagatctctctcgcgttgaagaacagtcgaatcgaagaga 342
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Db 1219 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1160

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Oy 403 agatctgaggaatacgttgcagatcgttaaacagaaagctgtgattac 457
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Db 1099 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1045

RESULT 2
US-08-947-823-1
Sequence 1, Application US/08947823
Patent No. 6114605
GENERAL INFORMATION:
APPLICANT: Williamson, Valerie M.
APPLICANT: Kaloshian, Isigouhi
APPLICANT: Yaghoobi, Jafar
APPLICANT: Bodeau, John
APPLICANT: Milligan, Stephen
TITLE OF INVENTION: Procedures and Materials for Confering
TITLE OF INVENTION: Pest Resistance in Plants
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/947, 823
FILING DATE: 09-OCT-1997
CLASSIFICATION: 800
APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/18802
FILING DATE: 09-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,191
FILING DATE: 10-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-070210US
TELECOMMUNICATION INFORMATION:

```

```

TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 51952 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-947-823-1

Query Match      5.3%; Score 49; DB 3; Length 51952;
Best Local Similarity 49.2%; Pred. No. 0.0053;
Matches 156; Conservative 0; Mismatches 160; Indels 1; Gaps 1;

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DB 32412 AAAATGCGTATCTGGATTATTTAAATCAATCATCTTTAAATGATATATCAAAATTTTAAATTA 32471
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 642 agtaacttcgatctcgaagaagatgagcacttggtggaagaagatacgaatggtgta 701
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 32472 ATTAACTTTTAAAAACAATAATAAAAAGCTAAAGTTTGTTTGACATGTTTGAAGGAAA 32531
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 702 aattgaatcgaatgaagaagacgatgatgaataagatgacatgtgtttccaaagaagt 761
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 32532 TATTAAACAATTTTAAATATATAAATGCTTGAAATGTTAATATTTTCTTAAACACT 32591
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 762 tatatcttctcgtcaataatcttgccttgatctttctttaacaataaccatgagt 821
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 32592 TTAAAGATTTCTTTATGTAAACATATGTAAATATTTGTTACAGAAATGACCACTAAATTC 32651
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 822 agatacttctcgcgaataatcaataacatgtaat-tcaactttggttgtaactcct 880
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 32653 GATCTTCATTATTGAAATATCTTTAAATGACGATATCAACATTTTAAATTAATTGAA 32711
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 881 gaggtgaactaatagat 897
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 32712 GAAATTTAAATTTACT 32728
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 3
US-08-487-826B-13/C
; Sequence 13, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chinitis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Knobbie Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsten, Ned

```

REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-487-826B-13

Query Match 4.8%; Score 44.4; DB 2; Length 19124;
Best Local Similarity 52.7%; Pred. No. 0.055;
Matches 96; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 725 tgaatgaatgaatgatactggtttccacaaagtactattttctctcgtgaataat 784
DB 15649 TTAATTTTATATATCATTTTATTAATAATAATTTTAAATTTTAAATTTTGAATA 15590
QY 785 ctctgcttgatcttctttaaacaatccaaatgagatctctcgcgaataac 844
DB 15589 ATCTTTTTCATTTTATTTCTATCAAAATTTATATTTTATTAATTTTATTTT 15530
QY 845 aataacatgaatcaacttctgttctactccctgaggaataataatgattcggtt 904
DB 15529 AAAAAATTTTCTCCTTTTATTTTATTTTATTTTAAATAAATTTTATTAAT 15470
QY 905 tt 906
DB 15469 TT 15468

RESULT 4
US-07-991-867B-41

Sequence 41, Application US/07991867B
Patent No. 5476781
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5476781e1 Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/991,867B
FILING DATE: 12-DEC-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991

ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UP114.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 1689 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-991-867B-41

Query Match 4.7%; Score 44; DB 1; Length 1689;
Best Local Similarity 52.1%; Pred. No. 0.033;
Matches 98; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 743 ttgtttcaccagaatctatttttctctcgtataatcttctgttattttct 802
DB 667 TTTTTCATATTCATCATATATATTTGTTCTGTAAACTATCTCTATTAATCT 726
QY 803 tttaacaatccaaatgagatatacttctcgcgaataacataacatgtaattcaac 862
DB 727 TTTTAAGACATATATAGCTATTAATATGTTTCTTAATTCCTTAATAATTAATTAATCTCC 786
QY 863 ttgtttctactctctgaggaataataatgattcggttttctcgaataaact 922
DB 787 ATTAATATATATCTCTCTTATATATCAATTAACATTTGGTCTAAGTAACCTATTAAT 846
QY 923 ataagtt 930
DB 847 ATTAAT 854

RESULT 5
US-08-544-332-41

Sequence 41, Application US/08544332
Patent No. 5935777
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5935777e1 Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gerard H. Bencen
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/544,332
FILING DATE: 07-DEC-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,867
FILING DATE: 07-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,755
FILING DATE: 19-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992

Query Match	4.7%;	Score 44;	DB 2;	Length 1689;
Best Local Similarity	52.1%;	Pred. No. 0.033;		
Matches 98;	Conservative 0;	Mismatches 90;	Indels 0;	Gaps 0;

```

RESULT 6
US-07-991-867B-1
Sequence 1, Application US/07991867B
Patent No. 5476781
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanich
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/991,867B
FILING DATE: 12-DEC-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992

```

```

Query Match          4.7%; Score 44; DB 1; Length 8457;
Best Local Similarity 52.1%; Pred. No. 0.054;
Matches 98; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 743 ttgtttccccaagaagtaactatattttctctgtlaataactcttgcttgatttct 802
      || |||||          || || || || || || || || || || || || ||
Db 7435 TTTTTCATTCATTCGATTCATATATATTTGTTCTGTTAACATTCGTTCAATTAATCT 7494

QY 803 tttaacaaatccaaatgtagatctctctctcgaataatcaataacatgtaaltcaac 862
      || || || || || || || || || || || || || || || || || ||
Db 7495 TTTTATGAGAAATATAGCTAATAATGTTCTCTTAATTCCTTAAATTAATTAACATTTC 7554

QY 863 ttgtgttgtaactccttgagtgtaattaatagatctggttttctcgatlaataaac 922
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Db 7555 ATTATTTATATATATCTCTCTTTATATATTCATTAACATTGGCTAAGTAACATTAATAATT 7614

QY 923 ataagtt 930
      || || ||
Db 7615 ATTAAATT 7622

RESULT 7
US-08-544-332-1
; Sequence 1, Application US/08544332
; Patent No. 5935777
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Hall, Richard L.
; APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expression System

```



```

NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESS: Gerard H. Bencen
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/544,332
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,867
FILING DATE: 07-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,755
FILING DATE: 19-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/627,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H.
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: UF114,C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8457 base pairs
TYPE: nucleic acid
STRANDEDNESS: ° double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Amsacta moorei entomopoxvirus
FEATURE:
NAME/KEY: CDS
LOCATION: complement (65..1459)
FEATURE:
NAME/KEY: CDS
LOCATION: 1474..2151
FEATURE:
NAME/KEY: CDS
LOCATION: complement (2239..2475)
FEATURE:
NAME/KEY: CDS
LOCATION: 2502..2987
FEATURE:
NAME/KEY: CDS
LOCATION: 3080..6091
FEATURE:
NAME/KEY: CDS
LOCATION: complement (6277..6768)
US-08-544-332-1

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Query Match	4.7%;	Score 44;	DB 2;	Length 8457;
Best Local Similarity	52.1%;	Pred. NO. 0.054;		
Matches 98;	Conservative	0;	Mismatches 90;	Indels 0;
			Gaps	0;

Oy	743	ttgttttcccaagaactactatattttcttcgaataaactttgtcgtttttct	802
Db	7435	TTTTTTTGCATATGCANCTATATTAATTTGTTCTGTAAACTATCGCTTCATTAACT	749
Oy	803	tttaacaaaalcccaatgtagatacttctctcgataaatacaatgtaattcaac	862
Db	7495	TTTATAGAACATATATACCTAATATATGTTCTCTTAATTCCTTAATAATTAATTAACCTTCC	755
Oy	863	tttgcgttgcactcccttggaagtaataatagatcogtgtttcttcgataataaact	922
Db	7555	ATTATTTATATATATATCTCTTTATATATCAATACATTTGGTCAAGTAACCTATTAATTT	761
Oy	923	ataagttt 930	
Db	7615	ATTAAATT 7622	

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RESULT      8
US-09-385-982--58
: Sequence 58. Application US/09385982
: Patent No. 626234
: GENERAL INFORMATION:
: APPLICANT: ENDEGE, WILSON O., ET AL.
: TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
: TITLE OF INVENTION: PRODUCTS: II
: FILE REFERENCE: CCDNA-260XX
: CURRENT APPLICATION NUMBER: US/09/385,982
: CURRENT FILING DATE: 1999-08-30
: EARLIER APPLICATION NUMBER: 09/328,111
: EARLIER FILING DATE: 1999-06-08
: EARLIER APPLICATION NUMBER: 60/117,393
: EARLIER FILING DATE: 1999-01-27
: EARLIER APPLICATION NUMBER: 60/098,639
: EARLIER FILING DATE: 1998-08-31
: NUMBER OF SEQ ID NOS: 544
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 58
: LENGTH: 471
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(471)
: OTHER INFORMATION: n = A,T,C or G
US-09-385-982-58

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Query March 4.58; Score 41.8; DB 4; Length 471;
Best Local Similarity 54.18; Pred. No. 0 077;
Matches 85; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

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DB 80 attgtattatttctctcttgataactcttttcataagattttgttaaaagattcaaa 139
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 819 tgtgataatcttctccgaataacaataacagtaattcaacttgytttacttc 878
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DB 140 atcaatgcacttgcgtcagaaaaataataataataacttaaatgttgcctctcc 199
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OY 879 ttgagtaattaattagattcgtgttttcttcgatta 915
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DB 200 ttgcatatttattcagaagatttttgytttgcacaa 236
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.RESULT 9
US-08-569-214-4/c
; Sequence 4, Application US/08569214
; Patent No. 6165469
; GENERAL INFORMATION:
; APPLICANT: MANN, BARBARA J.
; APPLICANT: PETRI, WILLIAM A.
; TITLE OF INVENTION: RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN
; SUBUNIT PEPTIDES AND REAGENTS SPECIFIC FOR MEMBERS OF THE

```



```

      FILING DATE: 6-NOV-1992
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/678,378
      FILING DATE: 1-APR-1991
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/305,566
      FILING DATE: 6-FEB-1989
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/165,667
      FILING DATE: 8-MAR-1988
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 08/042,847
      FILING DATE: 6-APR-1993
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/632,441
      FILING DATE: 21-DEC-1990
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/425,504
      FILING DATE: 20-OCT-1989
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/848,506
      FILING DATE: 6-MAR-1992
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/768,122
      FILING DATE: 27-SEP-1991
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/580,431
      FILING DATE: 7-SEP-1990
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/368,672
      FILING DATE: 20-JUN-1989
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/329,018
      FILING DATE: 24-MAR-1989
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 08/045,957
      FILING DATE: 12-APR-1993
      ATTORNEY/AGENT INFORMATION:
      NAME: Elmer, James Scott
      REGISTRATION NUMBER: 36,129
      REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (919)541-8614
      TELEFAX: (919)541-8689
      INFORMATION FOR SEQ ID NO: 36:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 12124 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: DNA (genomic)
      ORIGINAL SOURCE:
      ORGANISM: Cucumis sativus
      INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA
      IMMEDIATE SOURCE:
      CLONE: pBScucchrht5
      US-08-449-315-36

Query Match      4.1%; Score 37.8; DB 1; Length 12124;
Best Local Similarity 58.4%; Pred. No. 2.1;
Matches 66; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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Db 5750 AAATTAATTAATTAAGACTTTTGATTAATTAATTAAGTTAATTAACCTATGTGA 5691
Qy 761 ttatatatttccttcgtaacaatccttgcttggattttcttcaacaaat 813
Db 5690 TTAATAATTTGTAAATTAATTAAGTTATTTCTTAATATATTTTTTTTAAAAAAAT 5638

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Thu Jan 31 09:50:44 2002

us-09-574-735C-1.rni

Page 10

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DEFINITION Sequence 1 from Patent WO9914331.
ACCESSION A98054
VERSION A98054.1 GI:6781292
KEYWORDS
SOURCE
ORGANISM unidentified.
unclassified.
REFERENCE
1 (bases 1 to 932)
De,A.J. and De,V.L.
CYCLIN-DEPENDENT KINASE INHIBITORS AND USES THEREOF
JOURNAL Patent: WO 9914331-A 1 25-MAR-1999;
ALMEIDA JANICE DE (BE); LANDRIEU ISABELLE (BE)
FEATURES
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IEFDLENNNDDEDETETSMITYDUNKSEESMNDSSSAVEDVESRRRLKSLHETV
KEATLEDFQVAERDILRKLLCEGSMKNFDEKDEPLGGGHEWVKLNP"

BASE COUNT      289 a      125 c      254 g      264 t
ORIGIN

alignment_scores:
      Quality: 1064.00      Length: 209
      Ratio: 5.091
Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
US-09-574-735C-2 x A98054

Align seg 1/1 to: A98054 from: 1 to: 932

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17 lThrThrThrValLysArgArgLysMetGluGluGluValAspLeuV 34
|||||
136 TACGACGACGACGCTGAACGAGAGAGATGAGAGAGAGATGAGATTAG 185
34 alGluserArgIleIleuSerProCysValGlnAlaThrAsnArgly 50
|||||
186 TGCATCTAGATATATCTCTCTCGGTTACAGCGGAGAGATTCGCGGT 235
51 GlyIleValAlaArgAsnSerAlaGlyAlaSerGluThrSerValIle 67
|||||
236 GGAATTGTGGCGAGAAATTCAGCAGAGCGTCGCGAGACGAGTGTGTAT 285
67 eValArgArgArgAspSerProProValGluGluGluCysGlnIleGlu 84
286 AGTACGACGCGGAGATTCCTCGCGTTGAAGAACAGTGCMAATTCAGAG 335
84 LucIuAspSerSerValSerCysSerThrSerGluGluLysSerLys 100
|||||
336 AAGAAAGATTCTCGGTTCTGTCTACATCGCAAGAAATCGAA 385
101 ArgArgIleGluPheValAspLeuGluLysAsnGlnLysAspArgly 117
|||||
386 CGGAGAAATCGAATTTGTAGATCTTCAGGAAATACGCTGACATCGTA 435
117 uThrGluThrSerTrpIleTyrAspAspLeuAsnLysSerGluGluSerM 134
|||||
436 AACGAAACGTCGTGATTTACGATGATTTGAATACAGTACGAGATCGA 485
134 eLAsnMetAspSerSerValAlaValAluAspValGluSerArgArg 150
|||||
486 TGAACATGATTTCTCTCGGTCGCTGTGAAGATGATGATCTCGCCGC 535
151 ArgLeuArgLysSerLeuHisGluThrValLysGluAlaGluLeuGluAs 167
536 AGTTTAAGAGAGAGCTCCATGAGACGCTGAAGGAGCTGAGTTAGAGA 585
167 PhePheGlnValAlaGluLysAspLeuArgAsnLysLeuLeuGluCys 184
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586 TTTTTCAGGTGGCGGAGAAAGATCTCGGATTAAGTTGTTGGAATGT 635
184 eMetLysTyrAsnPheAspPheGluLysAspGluProLeuGlyGly 200
636 CTAAGAAGATTAACCTTCGATTCGAGAAAGATGAGCCACTTGTGTGAGGA 685
201 ArgTyrGluTrpValLysLeuAsnPro 209
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seq_name: gb_p1:ATT3A5

seq_documentation_block:
LOCUS ATT3A5 84196 bp DNA PLN 26-JAN-2000

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DEFINITION	Arabisidopsis thaliana DNA chromosome 3, BAC clone T3A5.
ACCESSION	AL132879
VERSION	AL132879.2
KEYWORDS	GI:6782244
SOURCE	thale cress.
ORGANISM	Arabisidopsis thaliana
REFERENCE	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eucotsids II; Brassicales; Brassicaceae; Arabidopsis.
AUTHORS	1 (bases 1 to 84196) Bloembergen, H., Mewes, H.W., Lemcke, K., Mayer, K.F.X., Quetier, F. and Salanoubat, M.
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 84196) EU Arabidopsis sequencing project.
AUTHORS	Direct Submission
TITLE	Submitted (25-JAN-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG. E-mail: bloembergen@biochem.mpg.de, myer@mpg.de, bloembergen@biochem.mpg.de
JOURNAL	Coordination: Marcel Salanoubat and Francis Quetier, Groupement d'Interet Public, Centre National de Sequencage - GENOSCOPE; 2 rue Gaston Creteil, BP191, 91006 Evry Cedex, France; http://www.genoscope.cns.fr
COMMENT	On Jan 27, 2000 this sequence version replaced gi:6434247. Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/ .
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exon	

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exon	complement(16014. .16470) /number=2
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Percent Similarity: 73.077      Percent Identity: 72.727

alignment_block:
US-09-574-735C-2 x ATT3A5
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17 lThrThrThrValValysArgArgGlyMetGluGluGluValAspLeu 34
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34 alGluserArgIleIleuserProCysValGlnAlaThrAsnArgGly 50

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67 eValArgArgArgAspSerProProValGluGluGluGluGluGlu 84
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84 lGluAspSerSerValSerCysCysSerThrSerGluIuLysSerLys 100
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12589 AAGAGATTCGTCGCTTCGTGTCTACATCGAAGAGAAATCGAAA 12638
101 ArgArgIleGluPheValAsp.Leu..... 108
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12639 CGGAGATTCGAATTTGTAGATCTTGAGGTGACAAAGCAATTAATTAT 12688
108 ..... 108
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125 PAspLeuAsnLys..... 129
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130 .....Ser 130
12839 ATCAGTAACAACATTTCTATAAATGCTTTGATTTTGTGTATAGT 12888
131 GluGluSerMetAsnMetAspSerSerSerValAlaValGluAspValG 147
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181 LeuGluCysSerMetLys..... 186
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LOCUS AX008796 755 bp DNA PAT 06-SEP-2000
DEFINITION Sequence 6 from Patent WO9964599.
ACCESSION AX008796
VERSION AX008796.1 GI:9996260
KEYWORDS
SOURCE
ORGANISM Arabidopsis thaliana

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 755)
Fowke, L.C., Wang, H. and Crosby, W.L.
Cyclin-dependent kinase inhibitors as plant growth regulators
Patent: WO 9964599-A 6 16-DEC-1999;
FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD (CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV SASKATCHEWAN TECHNOLOGIES (CA)

FEATURES

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Location/Qualifiers
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/db_xref="taxon:3702"

BASE COUNT 229 a 106 c 187 g 233 t
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US-09-574-735C-2 x AX008796 ..

Align seg 1/1 to: AX008796 from: 1 to: 755

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seq_name: gb_pl:AT094772

seq documentation block:

LOCUS AT094772 856 bp mRNA PLN 29-APR-1997
DEFINITION Arabidopsis thaliana cyclin-dependent kinase inhibitor protein (ICK1) mRNA, complete cds.
ACCESSION U94772
VERSION U94772.1 GI:2052501
KEYWORDS
SOURCE
ORGANISM
thale cress.
Arabidopsis thaliana

REFERENCE
1 (bases 1 to 856)
Wang, H., Fowke, L.C. and Crosby, W.L.
A plant cyclin-dependent kinase inhibitor gene
Nature 386 (6624), 451-452 (1997)

REFERENCE
2 (bases 1 to 856)
Wang, H., Fowke, L.C. and Crosby, W.L.
Submitted (20-MAR-1997) Plant Biotechnology Institute, 110
Gymnasium Place, Saskatoon, SK S7N 0W9, Canada

REFERENCE
TITLE
JOURNAL
Submitted (20-MAR-1997) Plant Biotechnology Institute, 110
Gymnasium Place, Saskatoon, SK S7N 0W9, Canada

FEATURES

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CDS

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ORIGIN

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Percent Similarity: 55.897 Percent Identity: 34.359

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94 ThrSerGluGluIySerIyArgArgIleGluPheValAspLeuGluGly 110
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166 ACGCAATGAAATATAGAGAAA.....GAATTAATACATCTGAGAGA 206
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304 AGTAATCCATGAGAAATTAATCATCGAATTGCAATCGCGGTAAAGA 353
144 uaspyalgluSerArgArgArgArgArgSerSerLeuHISgluThrVal. 160
354 ATCGTATGATTTGTTGTAGCGGAGAGAAAACGATGAGAGACGGTGA 403
161 .....Lysglu 162
404 CGCGGAGAGAGAGAGAGAGAGAAATGATGACGAGATGCCAACGAA 453
163 AlaGluegluAspPheglnValAlaGlulysAspleuArgAsnly 179
454 TCGGAAATTTGAAATTTTGTGGAAGCTGAGAAACAACTCAAGAAA 503
179 sleuenglucysersermetlystyrasnphesppheglulysaspglu 196
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LOCUS AX008791
DEFINITION Sequence 1 from Patent W0964599.
ACCESSION AX008791
VERSION AX008791.1 GI:9996255
KEYWORDS
SOURCE
ORGANISM

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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 904)
Folke, L.C., Wang, H. and Crosby, W.L.
Cyclin-dependent kinase inhibitors as plant growth regulators
Patent: WO 96/4599-A 16-DEC-1999; AGRICULTURE AND AGRI-FOOD CANAD
FOLKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRI-FOOD CANAD
(CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV
SASKATCHEWAN TECHNOLOGIES (CA)
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BASE COUNT 307 a 107 c 229 g 261 t
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quality: 209.00 length: 195
ratio: 1.917 gaps: 9
Percent Similarity: 55.897 Percent Identity: 34.359
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US-09-574-735C-2 x AX008791

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77 luGlucInGlnIleGluGluGluAspSerSerValSerCysCysSer 93
173 CC.....GTCGTCGTCATGATGAGATTTCGTCGTCGTGTAGTGA 213
94 ThrSerGluGluLysSerLysArgArgIleGluPheValAspLeuGlu 110
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144 uaspyalgluSerArgArgArgArgArgSerSerLeuHISgluThrVal. 160
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161 .....Lysglu 162
452 CGCGGAGAGAGAGAGAGAGAGAAATGATGACGAGATGCCAACGAA 501
163 AlaGluegluAspPheglnValAlaGlulysAspleuArgAsnly 179
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seq_name: gb_pl:AB029483

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seq_documentation_block: 927 bp mRNA PLN 11-JAN-2001
LOCUS AB029483
DEFINITION Pisum sativum cki mRNA for cyclin dependent kinase inhibitor,
complete cds.
ACCESSION AB029483
VERSION AB029483.1 GI:12081914
KEYWORDS cyclin dependent kinase inhibitor.
SOURCE Pisum sativum axillary bud cDNA to mRNA.
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Fabales; Fabaceae; Papilionoideae; Viciae;
Pisum.
1 (bases 1 to 927)
Shimizu-Sato, S. and Mori, H.
A cDNA from Pisum sativum encoding the cyclin-dependent kinase
inhibitor (CKI) homologue
Published only in Database (2001) In press
JOURNAL
REFERENCE
2 (bases 1 to 927)
Shimizu-Sato, S. and Mori, H.

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148 TCCTCGCGCGCTTTAGCGCTTGATAAATGTTCCGTACATCGGTGGA 197
71 gApSerPrProValGluGluGlnGlyGlnIleGluGluLysPser 88
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About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

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134 etAsmMetaspSerSerSerValAlaValaGluaSpValGluSerArgArg 150
508 TGAACATGATTTCTTCTCGGTGCTGTTGAAGATGTAAGTCTGCGCC 557
151 ArgLeuArgLysSerLeuHisGluThrValLysGluAlaGluLeuGluAs 167
558 AGGTTAAGGAAAGAGTCTCCATGAGACGGTGAAGAAAGTGAAGTGAAGA 607
167 pphhehgluValAlaGluLysAspLeuArgAsnLysLeuGluGlySer 184
608 TTTTTCAGGTGGCGAGAAAGATCTTCGAAATAGATTGTTGGAATGTT 657
184 ermEllystyranpheaSpheGluLysAspGluProLeuGlyGly 200
658 CTAATGAGATTAACCTTCGATTCGAGAAAGATGACCACTTGTTGAGAGA 707
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seq_documentation_block:
ID AAX25015 standard; cDNA; 932 BP.

AC AAX25015;

DF 05-JUL-1999 (first entry)

DE Arabidopsis cyclin-dependent kinase inhibitor FL39 cDNA clone.

KW Cyclin-dependent kinase inhibitor; CDK inhibitor; CKI; CDKI;

KW FL39; plant development; transgenic plant; cell cycle;

KW growth regulator; herbicide; ds.

OS Arabidopsis thaliana.

XX Key Location/Qualifiers

FT CDS 86..715

FT polyA_signal 915..920

FT misc_feature 305..932

FT /tag- C

FT /note- "this region of the sequence is specifically

FT claimed in Claim 1(c)"

FT MO9914331-A2.

XX 25-MAR-1999.

XX 16-SEP-1998; 98WO-EP05895.

XX 24-DEC-1997; 97EP-020411.

XX 16-SEP-1997; 97EP-020838.

XX (CROP-) CROPESTIGN NV.

XX De Almeida J, De Veylder L, Inze D, Landrieu I;

XX WPI: 1999-229535/19.

XX P-PSDB: AAM98179.

XX DNA encoding inhibitor of cyclin-dependent kinase

XX Claim 1b; Page 72-74; 88pp; English.

XX This is the DNA sequence of FL39, a cDNA clone that encodes a new
CC cyclin-dependent kinase (CDK) inhibitor (see AAM98179) of Arabidopsis
CC thaliana. New plant products with a putative CDK inhibitory
CC function were screened by using a two-hybrid system with CDC2aa1
CC protein as bait and a library made from an RNA mixture of A.
CC thaliana cell suspensions harvested at the early exponential,
CC exponential, early stationary and stationary phases. Positive
CC clones LDV39, LDV66 and LDV15 were obtained. Clone FL39 was
CC isolated from a flower cDNA library using partial clone LDV39 as
CC probe. Clone FL66 (see AAX25015) was similarly obtained using LDV66.
CC Another CDK inhibitor, ALPCDK1 (see AAX25018), was obtained from
CC alfalfa. Results established that several CDK inhibitors exist
CC in plants and that these inhibitors are expressed at different
CC time points and may have different functions during the development
CC of the plant. CDK inhibitors, nucleic acids, antibodies, promoter
CC sequences, related recombinant DNA and vectors are all useful: for
CC diagnosis (no details); for modulating the cycle, division and/or
CC growth of plant cells; for altering activity of CDK; for modulating
CC growth inhibition in plants caused by environmental stress; for
CC inducing male or female sterility; for altering cell division
CC progression in plants, bacteria, fungi, insect and animal cells;
CC and to screen for agonists or antagonists that are potentially
CC useful as growth regulators or herbicides. Plants of any sort can
CC be treated, e.g. to alter their size or resistance to disease.
XX Sequence 932 BP; 289 A; 125 C; 254 G; 264 T; 0 other:

alignment_scores:

Quality: 1064.00

Ratio: 5.091

Percent Similarity: 100.000

Percent Identity: 100.000

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167 pPhePheGlnValAlaGluLysAspLeuArgAsnLysLeuLeuGluCys 184
586 TTTTTCAGGTGGCGGAGAAAGATCTCGGAAATAGTTGTTGGAATGTT 635
184 erMetLysTyrAsnPheAspPheGluLysAspGluProLeuGlyGly 200
636 CTATGGAAGTATTAAGTTCGATTCGAGAAAGATGAGCCACTTGTTGAGAGA 685
201 ArgTyrGluTyrPValLysLeuAsnPro 209
686 AGATACGAGTGGGTTAAATTGAAATCCA 712

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ID AAC85204 standard; DNA; 809 BP.
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AC AAC85204;
XX
DT 22-MAR-2001 (first entry)
XX
DE Plant D-like cyclin inhibitor BRO3 coding sequence.
XX
KM Plant; D-like cyclin inhibitor gene; BRO4; hyperplastic; variant;
KW growth rate; dividing cells; inactivation; protoplast; seed;
KM root cell; meristem; leaf; ss.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT CDS 69..620
FT /tag= a
FT /product= BRO3
XX
PN WO200069883-A1.
XX
PD 23-NOV-2000.
XX
PF 15-MAY-2000; 2000WO-US13379.
XX
PR 14-MAY-1999; 99US-0134373.
XX
PA (HUTC-) HUTCHINSON CANCER RES CENT FRD.
XX
PI Roberts J, Kelly B;
XX
DR MPI; 2001-024998/03.
XX
DR P-PSDB; AAB47004.
XX
PT Functionally inactivating expression of plant D-like cyclin inhibitor
PT gene for producing a hyperplastic variant plant, modulating the growth
PT and/or yield of plants, and increasing the proportion of dividing cells
XX
XX
XX Example 1; Page 39-40; 50pp; English.
XX
XX The sequence given in AAC85204 represents a plant D1 cyclin
XX inhibitor gene, BRO3. This sequence was isolated using a yeast two
XX hybrid screen. The BRO3 protein was found to contain a seven amino
XX acid sequence cyclin binding domain similar to that of BRO1, BRO2
XX and BRO4 (See also AAB47005-6). This sequence is homologous to a
XX sequence present in a D-like cyclin inhibitor gene and when integrated
XX at the corresponding locus, functionally inactivates plant D-like
XX cyclin inhibitor protein expression. The BRO4 coding sequence may
XX be used to produce a hyperplastic variant plant, increase the growth
XX rate of a plant, or increase the proportion of dividing cells in a
XX plant cell population, relative to a wild-type plant, by functionally
XX inactivating the expression of a plant D-like cyclin inhibitor
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CC gene in a plant. BRO4 is useful for increasing the proportion of
CC dividing cells in a plant cell population comprising protoplast,
CC seeds, root cells, meristem cells or leaf cells.
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Ratio: 5.109 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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65 GAAAGATGAGGAGGAGAGATGATTTAGTGGAATCTAGGATTAATCTGCTC 114
42 roCysValGlnAlaThrAsnArgGlyGlyIleValAlaArgAsnSerAla 58
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115 CGTGTGACAGCGACGACGATCGCGTGAATTTGCGGACGAAATTCAGCA 164
59 GlyAlaSerGluThrSerValValIleValArgArgArgAspSerProp 75
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165 GGACCGTCGGAGACGAGTGTGTATAGTACGACGCGAGATCTCTCC 214
75 oValGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 92
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215 GGTGGAAGAACAGTGTCAATCGAAGAGAGATCTCGGTTTCGCTT 264
92 ySerThrSerGluGluLysSerLysArgArgIleGluPheValAspLeu 108
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265 GTTCTACATCGGAAGAGAAATCGAAACGAGAAATCGAATTTGTTGATCTT 314
109 GluGluAsnAsnGlyAspAspArgGluThrGluThrSerTrpIleTyrAs 125
|||||
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125 pAspLeuAsnLysSerGluGluSerMetAsnMetAspSerSerSerVala 142
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365 TGATTGAATTAAGATGAGGATGATGAACATGATTCCTTCGGGTGG 414
142 lAlaValGluAspValGluSerArgArgArgLeuArgLysSerLeuHisGlu 158
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415 CTGTTGAAGATGTAGACTTCGCCGCGGTTTAAGAGAGAGACTCTCCAGAG 464
159 ThrValLysGluAlaGluLeuGluAspPhePheGlnValAlaGluLysAs 175
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465 ACGGTGAAGGAAAGCTGAGTTAGAAAGACTTTTTCAGCTGCGGGAAGA 514
175 pLeuArgAsnLysLeuLeuGluCysSerMetLysTyrAsnPheAspPheG 192
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515 TCTTGGAAATTAAGTTGTTGAAGTCTTATGAAGTAACTTCGATTTCG 564
192 lLysAspGluProLeuGluGlyGlyArgTyrGluTyrPValLysLeuAsn 208
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ID AA229416 standard; cDNA; 755 BP.
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99 ACGGAGCCGGAGAAATGTTTATGTTATCGAAATCAACGCTTGTCT 148
77 LuGIuGIuGlnGlnIleGIuGIuAspSerSerValSerCysSer 93
149 CC.....GTCTCGCTGATATGAGATTGCTGCTGTGTGAGTGA 189
94 ThrSerGIuGIuLysSerLysArgArgIleGIuPheValAspLeuGI 110
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110 uAsnAsnGlyAspAspArgGluThrGluThrSerTrpIle..... 123
231 GGAACAT...AAAGTGTGTGACACTGAAACGTCGATCGACGGGTA 277
124TyrAspAspLeu 127
278 CGAAGAGGAACCTTTTGAATATCGAGAGAGAGAGAAAGAAATTA 327
128 AsnLysSerGIuGIuSerMetAspMetAspSerSerValAlaValGI 144
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161LysGlu 162
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478 TCGGAATTTGAAGATTTTGTGTGAGACGTGGAACCACTCAAGAA 527

179 sLeuLeuGIuCysSerMetLysTyrAsnPheAspPheGIuLysAspGluP 196
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DT 17-OCT-2000 (first entry)
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XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
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Quality: 209.00 Length: 195
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Percent Similarity: 55.897 Percent Identity: 34.359

alignment_block:

US-09-574-735C--2 x AAC36958 ..

Align seg 1/1 to: AAC36958 from: 1 to: 780

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   77 IuglGlnCysGlnIleGluGlnGluAspSerSerValSerCysCysSer 93
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233 GGAAGAT...AAGATGCTGACACTGAAACGTCGACGATCGACGGGTA 279
   124 .....TyrAspAspLeu 127
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380 ATCGTTGATGATTGTTGTTGACCGGAGAGAAACATGAGAGACGGTGA 429
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   :|||:|||||
430 CCGGAGAGAGAGAGAGAGAGAGAAATTCATGACGAGATGCCAACGAA 479
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   :|||:|||||:|||||:|||||
480 TCGGAAATTTGAAGATTTTGTGGAAGCTGAGAAACAACTCAAGAAAA 529
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530 ATTC.....AAGAGAGAGATCAATTTTCGATTTTCGAGAAAGAGAGC 570
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seq.name: /SID52/gcgdata/geneseq/geneseg/NA2000.DAT:AA229415

seq_documentation_block:

ID AA229415 standard; cDNA; 904 BP.

XX AA229415;

XX 29-FEB-2000 (first entry)

XX Arabidopsis thaliana CDK inhibitor, ICK1 encoding cDNA.

XX Cyclin-dependent kinase inhibitor; CDK; Interactor of Cdc2 kinase 1;

KW ICK1; Cdc2a; D-class cyclin; CycD1; CycD2; morphogenesis;

KW antisense construct; tissue-specific promoter; transgenic plant;

KW male sterility; ds.

XX Arabidopsis thaliana.

XX Key Location/Qualifiers

FT CDS 55..630

FT /tag= a

FT /product= "ICK1"

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FT misc_feature 40..42
FT /tag= c
FT /note= "In-frame stop codon"
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FT /tag= d
FT /note= "In-frame stop codon"
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XX W09964599-A1.
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XX 16-DEC-1999.
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XX 08-JUN-1999; 99MO-CA00532.
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XX 08-JUN-1998; 98CA-2235978.
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XX
XX (MIAC ) AGRIC & AGRIFOOD CANADA.
XX (UTSA-) UNIT SASKATCHEWAN TECHNOLOGIES INC.
XX (CANA ) NAT RES COUNCIL CANADA.
XX
XX Wang H, Fowke LC, Crosby WL;
XX
XX WPI: 2000-097540/08.
XX
XX P-PSDB; AAY44335.
XX
XX Modifying plant cell development using nucleic acid encoding inhibitor
XX of cyclin-dependent kinase, or corresponding antisense sequence, e.g.
XX for inducing male sterility -
XX
XX Claim 5; Fig 1; 58pp; English.
XX
XX The present sequence is a cDNA encoding A. thaliana Cyclin-Dependent
XX kinase (CDK) inhibitor, ICK1. Interactor of Cdc2 kinase 1 (ICK1)
XX interacts with Cdc2a, D-class cyclins, CycD1, CycD2 and CycD3. Growth,
XX morphogenesis, multiplication, enlargement, differentiation and
XX maturation of plant cells can be modified by transforming them with
XX nucleic acid encoding CDK inhibitor or antisense construct complementary
XX to the inhibitor gene, operably linked to a tissue-specific promoter.
XX The transgenic plants exhibit alteration of traits such as petals, male
XX sterility and ability to set seeds.
XX
XX Sequence 904 BP; 307 A; 107 C; 229 G; 261 T; 0 other;
XX

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alignment_scores:

Quality: 209.00 Length: 195
Ratio: 1.917 Gaps: 9
Percent Similarity: 55.897 Percent Identity: 34.359

alignment_block:

US-09-574-735c-2 x AA229415 ..

Align seg 1/1 to: AA229415 from: 1 to: 904

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173 CC.....GTGCTCGGTGATATGATGATTCATGCTCTTGTAGTGA 213
   94 ThrSerGluGluGluSerLysArgArgIleGluPheValAspLeuGluG 110
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214 AGCATGATGATTAAGAGAAA.....GAATTAATACATCTGAGAGA 254

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188 snpheasphegluylaspgluproleuglygllyargtyrglutrp 204
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seq_documentation_block:
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 XX
 AC AAC85201;
 XX
 DT 22-MAR-2001 (first entry)
 XX
 DE Plant D-like cyclin inhibitor BRO4 coding sequence.
 XX
 KW Plant; D-like cyclin inhibitor gene; BRO4; hyperplastic; variant;
 KM growth rate; dividing cells; inactivation; protoplast; seed;
 KW root cell; meristem; leaf; ss.
 XX
 OS Arabidopsis thaliana.
 XX
 FH Key Location/Qualifiers
 FT CDS 36..626
 FT /*tag= a
 FT /product= BRO4
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 PN WO200069883-A1.
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 PD 23-NOV-2000.
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 PF 15-MAY-2000; 2000WO-US13379.
 XX
 PR 14-MAY-1999; 99US-0134373.
 XX
 PA (HUTC-) HUTCHINSON CANCER RES CENT FREED.
 XX
 PI Roberts J, Kelly B;
 XX
 DR WPI: 2001-024998/03.
 DR P-PSDB: AAB47001.
 XX
 XX
 PT Functionally inactivating expression of plant D-like cyclin inhibitor
 PT gene for producing a hyperplastic variant plant, modulating the growth
 PT and/or yield of plants, and increasing the proportion of dividing cells
 XX
 PS Claim 16; Page 41; 50pp; English.
 XX
 XX The sequence given in AAC85201 represents a plant D-like cyclin
 CC inhibitor gene, BRO4. This sequence may be used to produce a
 CC hyperplastic variant plant, increase the growth rate of a plant,
 CC or increase the proportion of dividing cells in a plant cell
 CC population, relative to a wild-type plant, by functionally
 CC inactivating the expression of a plant D-like cyclin inhibitor
 CC gene in a plant. This sequence is homologous to a sequence present
 CC in a D-like cyclin inhibitor gene and when integrated at the
 CC corresponding locus, functionally inactivates plant D-like cyclin
 CC inhibitor protein expression. BRO4 is useful for producing
 CC hyperplastic variant plants, increasing the growth rate of a plant
 CC and for increasing the proportion of dividing cells in a plant cell
 CC population comprising protoplast, seeds, root cells, meristem cells
 CC or leaf cells.
 CC
 SO Sequence 626 BP; 202 A; 131 C; 156 G; 137 T; 0 other;

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 Ratio: 1.273 Gaps: 13

Percent Similarity: 65.566 Percent Identity: 30.660

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 US-09-574-735c-2 x AAC85201 ..

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 45 AGAAGAGAGAGCTTGCAGAGAAAGCTTCAAGCACAAGCTTCCACCACT 94
 22 llysargarglysmetgluugluvalasp...leuvalgluSerargi 38
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 233 AGAAGT.....GATCAGCTCTCGA 252
 88 erValSerCys...CysSerThrSerGluGluys.....SerLysArg 101
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 253 GTATCAGCTCCGCTTGTTCACCGATGAGAAAGAAATCGCAGAAC 302
 102 ArgIleGluPhe...ValAspLeuGluGluAsnGlnGlyAspArgGlu 117
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 303 AGTTCGTCGTTGGTGTGATCTGAGATCATCA...ATCGAAACCGA 349
 117 uThrGluThrSer...TrpIleTyraSpAspLeuAsnLys.....Serg 131
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 350 AACCGAAACCTCAACATTCATCACACGCAATTCAGAAAAGACGAGTC 399
 131 lgluSerMetAsnMetAspSerSerSerValAlaValGluAspValGlu 147
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 400 CACTGACTGAGCGTTTGGAGAAACGACACAGAAATGGAATCATCATCG 449
 148 SerArgArgArgLeuArgLysSerLeuHisGluThrValLysGluAlaG 164
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 XX
 DT 29-FEB-2000 (first entry)
 XX
 DE Arabidopsis thaliana CDK inhibitor, ICN2 encoding cDNA.
 XX
 KW Cyclin-Dependent kinase inhibitor; CDK; Interactor of Cyclin 2;
 KW ICN2; cdc2a; D-class cyclin; CycD1; CycD2; morphogenesis;
 KW antisense construct; tissue-specific promoter; transgenic plant;


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99 .....SerLysArgArgIleGluPheValAspLeuGluGluAsnGly 113
113 yAspAspArgGluThrGluThrSerTrpIleTyrAspAspLeuAsnLys 130
222 TTACATTGGTGGTTGAG.....TATGTCGATGCCACAGAT 259
130 eRGLGluSerMetAsnMetAspSerSerSerValAlaValGluAspVal 146
260 CTGGCAGATGCTC.....GTT 276
147 GluSerArgArgArgLeuArgLysSerLeuHisGluThrValGluAla 163
277 GAATTGAACGAGAGGTTGAACAGGT.....GG 305
163 aGluLeuGluAspPhePheGluValAlaGluLysAspLeuArgAsnLysL 180
306 TTTTATCAGCCACGTTTGTGATGTTGTCAGCAAGAAATTGAAG..... 350
180 euLeuGluCysSerMetCysTyrAsnPheAspPheGluLysAspGluPro 196
351 ..TTGGAAATGTTCTATGAAGTAACTTCGATTCGAGAAAGATGAGCCA 398
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XX AAA95288;
AC
XX
XX 17-JAN-2001 (first entry)
XX
XX Soybean cyclin-dependent kinase inhibitor coding sequence #3.
KM Soybean; cyclin-dependent kinase inhibitor; cell cycle; cell division;
XX CKI; cell growth; herbicide; ss.
OS Glycine max.
XX
FH Key Location/Qualifiers
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FT /product= "CDKI"
XX
XX W0200060087-A2.
XX
XX 12-OCT-2000.
XX
XX 06-APR-2000; 2000MO-US09106.
XX
XX 07-APR-1999; 99US-0128192.
XX
XX (DUPO ) DU FONT DE NEMOURS & CO E I.
XX
XX Klein TM, Weng Z, Cahoon RE;
XX
XX WPI: 2000-679375/66.
XX
XX P-PSDB: AAB27254.
XX
XX Cyclin dependent kinase inhibitor sequences, useful for identifying
XX herbicides and plant growth inhibitors
XX
XX Claim 2; Page 49-50; 58pp; English.
XX
XX The present sequence is the coding sequence for the soybean
XX cyclin-dependent kinase inhibitor (CDKI). It was isolated by searching a
XX soybean pod cDNA library for sequences similar to those encoding the

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CC CDKI from Chenopodium rubrum, Caenorhabditis elegans and Arabidopsis
CC thaliana. CDKI is involved in the cell cycle, and may promote or inhibit
CC cell division and growth. The coding sequence and the protein it encodes
CC are useful in the production of transgenic plants which produce increased
CC or decreased amounts of the CDKI protein, in the identification of
CC herbicides, in genetic and physical mapping and in the isolation of the
CC CDKI gene in other organisms.
XX
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211 TGAACCATCATCTCAAGAAAGATGATGACCAACACTACTAAC..... 253
35 LysSerArgIleLeuSerProCysValGluAlaThrAsnArgGlyGly 51
254 .....CAAGAGCCAAACTCTCAAGACTCCGAGA..... 283
52 IleValAlaArgAsnSerAlaGlyAlaSerGluThrSerValIleVal 68
284 .....ACGAGTCTTCCTCCGCTGCATCAACACGACGCGTACGAGAT 327
68 LArgArgArgAspSerProProValGluGluGlnGlyGlnGluGluG 85
328 GGTTCAGCCGCTGTCGCGGAGATGGTTCAGCAACCTCCGTAGGCCCA 377
85 LysSerSerVal.....SerCysCysSerThr.....SerGluGlu 97
378 CCTCCAGTGAATTCGGGGCTGCTGCTCCAGCAAGGATCCATTGGC 427
98 LysSerLysArgArgIleGluPheValAspLeuGluGlu..... 110
428 CTCGATCAGACGACGATCAAGCTTAGATCTGAGGTGAGCGACGCGCA 477
111 .....AsnAsnGlyAspAspArgGluThrGluThr 121
478 ACTGGAACGTCGACGTCGCAATGTGTGTCATGAAATTGAGAGAGA.... 523
121 eRTrpIleTyrAspAspLeuAsnLysSerGluGluSerMetAsnMetAsp 137
524 .....GAGATGAACGTTCCAGCGAG...CTGCGCGAGAT 556
138 SerSerSerValAlaValGluAspValGluSerArgArgArgLeuArgly 154
557 TCTCAGAGACCGGAGCCCAATGAGATCAATCTCAGCGTGTTCATCAA 606
154 sSerLeuHisGluThrValLysGluAlaGluLeuGluAspPhePheGlu 171
607 GGCA...AAGCCATCCCTAACCGAATTGAGCTCGGAGATTCCTGGCG 653
171 AlaGluLysAspLeuArgAsnLysLeuLeuGluLysSerMetLysTyr 187
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188 AsnPheAspPheGluLysAspGluProLeuGlyGlyArgTyrGluTr 204
695 AATTATGATATGTTTAAAGACGATACCGGTG...GAAGACGCTACGAGTG 741

```


Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.

1 (bases 1 to 754)
 Fedorova,M., Pierson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Town,C.D., Van Aken,S., Utterback,T., Cho,J. and Fraser,C.M.
 ESTs from one month old nitrogen-fixing root nodules of Medicago truncatula, 2001

JOURNAL
 Unpublished (2001)
 Contact: Carroll P. Vance
 Department of Agronomy and Plant Genetics
 University of Minnesota
 411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
 Tel: 612 625 5715
 Fax: 651-649-5058
 Email: vance004@maroon.tc.umn.edu
 University of Minnesota name: M382960e TIGR sequence name: MTC00777K More information is available at: http://www.medicago.org
 Seq primer: Skmod (CTA gAA CTA gTg gAT CC).

FEATURES
 Location/Qualifiers
 1..754
 /organism="Medicago truncatula"
 /cultivar="genotype A17"
 /db_xref="taxon:3880"
 /clone="PGVN-66M9"
 /clone_1lb="GVN"
 /tissue="type=N2-fixing root nodules"
 /dev_stage="effective root nodules harvested one month post inoculation with Sinorhizobium meliloti"
 /lab_host="E. coli strain XL0R"
 /note="Vector: pBluescript SK-; Site.1: EcoRI; Site.2: XhoI; cDNA was prepared from polyA+ enriched RNA from effective root nodules harvested one month post inoculation with Sinorhizobium meliloti. The cDNA was directionally ligated into the uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XL0R cells."

BASE COUNT
 210 a 189 c 159 g 196 t

ORIGIN

alignment_scores:
 Quality: 131.00 Length: 223
 Ratio: 1.129 Gaps: 12
 Percent Similarity: 52.018 Percent Identity: 28.251

alignment_block:
 US-09-574-735C-2 x BG581898 ..

Align seg 1/1 to: BG581898 from: 1 to: 754

5 ArgArGArGluArGAspValValGluGluAsnGlyValThrThrTh 21
 |||||
 84 CGAGTCCGCCGCCGAT.....AATGAAATCACCACATCTCACT 121
 21 rVallysrArg.....LysMetGluGluGlu 31
 |||||
 122 CCACCGCGCTGCTCCGACACGTCGCAAAACCTCGCACTCCGAAA 171
 31 aAlaPleuValGluSerArg.....IleIleLeuSerProCysValGln 45
 |||||
 172 TCTCC...GCCGAATCACCTGATTCCTTCCTTCCTCGACGCTCCG 218
 46 AlaThrAsnArgGlyGlyIleValAlaArgAsnSerAlaGlyAlaSer 62
 |||||
 219 CCGCGCGCTCGTAAGTTCCTCCGCCCTTCACACTCGCAAGAGACG 268
 62 urhSerValValIleValArg.ArgArGAspSerProValGluGlu 78
 |||||
 269 GTTCTCCGGAATAATCCAGCTCTG..... 294

79 GlnCysGlnIleGluGluGluAspSerSerValSerCysSerThrSe 95
 ::|||
 295 GAATGTCGGTGGAAAA.....TTGGAAATTTCTGTGCTGA 332
 95 rGluGluLysSerLysArgArgIleGluPheVal..... 106
 |||||
 333 AGAAGAGAAATGAGATGATGATGATTCGCTGTAAGTTCTTTTG 382
 107AsPleuGluGluAsnGlyAspAspArgGluThrGluThrSer 121
 ::|||
 383 GTGAAATTTTCGACAGATGATGATGATGATGATGATGATGATGATG 432
 122 TrpIleTyraPaspPleuAsnLysSerGluGluSerMetAsnMetAspSe 138
 ::|||
 433ACACCTGTGATTTAAATCAGGATTC 458
 138 rSerSerValAlaValGluAspValGluSerArgArgArgLeuArgLys 155
 |||||
 459 AAGTGTCTATTCATACCCCTGTTCAACCAAGCAAGCAAGCAACACA 508
 155 erLeuHISGlu.....ThrValLysGluAlaGluLeuGlu 166
 ::|||
 509 TTATTCAGAAACACATGCAGAAATACTCCACACTAATGAAGTGGAT 558
 167 AspPhePheGluValAlaGluLysAspLeuArgAsnLysLeuLeuGluCy 183
 ::|||
 559 GAATTCCTTGCCCTTGGCAGAGACGACACAGACATTTATTTATGAA.. 606
 183 sSerMetLysTyraPaspPheGluLysAspGluProLeuGlyGly 200
 |||||
 607AAGTACATTTTGAATGATGATGATGATGATGATGATGATG 646
 200 lYArGTYGluTrpVal 205
 |||||
 647 GACGCTACGAATGGCTC 663

seq_name: gb_est2:BG581898

seq_documentation_block:
 LOCUS BG581898 766 bp mRNA EST 11-APR-2001
 DEFINITION EST483735 GVN Medicago truncatula cDNA clone pGVN-66M24 5' end,
 mRNA sequence.
 ACCESSION BG581898
 VERSION BG581898.1 GI:13597062
 KEYWORDS EST.
 SOURCE barrel medic.
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
 Medicago.
 1 (bases 1 to 766)
 Fedorova,M., Pierson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Town,C.D., Van Aken,S., Utterback,T., Cho,J. and Fraser,C.M.
 ESTs from one month old nitrogen-fixing root nodules of Medicago truncatula, 2001

JOURNAL
 Unpublished (2001)
 Contact: Carroll P. Vance
 Department of Agronomy and Plant Genetics
 University of Minnesota
 411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
 Tel: 612 625 5715
 Fax: 651-649-5058
 Email: vance004@maroon.tc.umn.edu
 University of Minnesota name: M383061e TIGR sequence name: MTC08484K More information is available at: http://www.medicago.org
 Seq primer: Skmod (CTA gAA CTA gTg gAT CC).

FEATURES
 Location/Qualifiers
 1..766
 /organism="Medicago truncatula"
 /cultivar="genotype A17"
 /db_xref="taxon:3880"

Site 2: NotI. This cDNA library was constructed from mRNA isolated from hypocotyl and plumule tissues of seeds germinated for three days of the cultivar Williams.

Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a NotI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by digestion with EcoRI and NotI. The cDNA fragments were directionally cloned into the EcoRI-NotI restriction site of the pT73-Pac vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker.

BASE COUNT 170 a 158 c 145 g 147 t 3 others
ORIGIN

alignment_scores:
Quality: 114.00 Length: 126
Ratio: 1.629 Gaps: 6
Percent Similarity: 55.556 Percent Identity: 33.333

alignment_block:
US-09-574-735C-2 x BE347049 ..

Align seg 1/1 to: BE347049 from: 1 to: 623

```

87 SerSerValSerCysCysSerThrSerGluGluSerLysArgArgI1 103
||||| ||||||||| ||||| ||||| ||||| ||||| |||||
294 TCCGATCCCTCTGCTGCGAGCTCCAGCCAGCTTTCAGACCTCCACTCGT 343
103 egluPheValaspLeuGluGluAsnGlyAspAspArgGluThrGluT 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
344 GCCG...TCAGATTCGACAGACCAAGGTTTCGAACGCTAGACAGCTCA 390
120 hrSerTrpIleTyrAspAspLeuAsn.....Lys 129
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
391 CCAGCCTCAATTCAATCGTTCAGTGTGAGTCTTTCGCGAGAC 440
130 SerGluGluSer...MetAsnMetAspSerSerSerValAlaValGluAs 145
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
441 TCGAGGAGATCGCGCATGATTCGCGCGAGAGTTCGCGCGGCTCTGAN 490
145 pValGluSerAArgAArgLeuAArgLysSerLeuHISgluThrValLysG 162
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
491 AGTG.....AGACGCCGCCGA 507
162 luAlaGluLeuGluAspPheGlnValAlaGluLysAspLeuAArgAsn 178
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
508 AGCGGAGATCGAGAGAGTTCGCGAGTGGCGANAGTACGACGCAAAA 557
179 LysLeuLeuGluCysSerMetLysTyrAsnPheAspPheGluLysAspG 195
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
558 CCGTTCACAGAG.....AAGTACAACTTGTATTTGTTAGAGATT 598
195 uProLeuGlyGlyAArgTyrGluTTP 204
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
599 GCCGTTG...GAGGTCGCTACCACTGG 623
seq_name: gb_est2:BG841133

```

seq_documentation_block:
LOCUS BG841133 604 bp mRNA EST 29-MAY-2001
DEFINITION MEST18-A04.T3 ISUM4-TN zea mays cDNA clone MEST18-A04 3', mRNA
sequence.
ACCESSION BG841133
VERSION BG841133.2 GI:14243442
KEYWORDS EST.
SOURCE zea mays.
ORGANISM zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
Clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 604)

AUTHORS Qiu, F., Guo, L., Ashlock, D.A., Wen, T.J. and Schnable, P.S.
TITLE Expressed Sequence Tags from B73 Maize Seedlings and Silks
JOURNAL Unpublished (2001)
COMMENT On May 25, 2001 this sequence version replaced gi:14207455.
Contact: Patrick S. Schnable

Schnable Laboratory
Iowa State University
6405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu

PCR Primers
FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
Location/Qualifiers

FEATURES

source

1..604
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="MEST18-A04"
/clone_1b="ISUM4-TN"
/tissue_type="Seedling and silk"
/lab_host="DH10B"
/note="Vector: pT73PAC; Site_1: EcoRI; Site_2: NotI;
ds-cDNA molecules were generated as follows. First-strand
cDNA was prepared from oligo-dT selected mRNA by priming
with a NotI oligo-dT primer (5',
AACTGACAGATTCGCGCGCGCGAGATTTTCTTTTCTTTT). The
resulting DNA:RNA hybrid was treated with RNase H and used
as a template for DNA Pol-I-catalyzed second strand
synthesis. After the addition of EcoRI adapters, the
ds-cDNAs were digested with NotI and size-selected. The
resulting molecules were directionally cloned into the
EcoRI and NotI sites of the pT73PAC vector. The library
then went through one round of normalization to Cot value
of 5 based on the methods of Marcelino Bento Soares (Genome
Research 6: 791-806, 1996)."

BASE COUNT 120 a 174 c 170 g 140 t
ORIGIN

alignment_scores:
Quality: 113.50 Length: 46
Ratio: 3.243 Gaps: 1
Percent Similarity: 76.087 Percent Identity: 43.478

alignment_block:
US-09-574-735C-2 x BG841133/rev ..

Align seg 1/1 to reverse of: BG841133 from: 1 to: 604

```

164 GluLeuGluAspPheGlnValAlaGluLysAspLeuAArgAsnLysLe 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
405 GAGGTGGAGGGGCTTCGCGCGACGAGGCGCGCATGCGCGCGCGCTT 356
180 uLeuLysSerMetLysTyrAsnPheAspPheGluLysAspGluProL 197
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
355 C.....GGGTCAAGTACAACTATGACCTGTCACAGAGCGCTCCCA 315
197 euGlyGlyAArgTyrGluTTPValLysLeuAsnPro 209
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
314 TGGACGGCGCGCGTACAGATGCGGTCCGAGTGGCGGCC 277

```

seq_name: gb_est1:A1728644
seq_documentation_block:
LOCUS A1728644 646 bp mRNA EST 11-JUN-1999
DEFINITION BNUGH11291 six-day cotton fiber Gossypium hirsutum cDNA 5' similar
to (AJ002173) cyclin-dependent kinase inhibitor protein
[Chenopodium rubrum], mRNA sequence.
ACCESSION A1728644
VERSION A1728644.1 GI:5047496

KEYWORDS EST.
SOURCE upland cotton.
ORGANISM Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
REFERENCE 1 (bases 1 to 646)
AUTHORS Blewitt, M., Matz, E.C., Davy, D.F. and Burr, B.
TITLE ESTs from developing cotton fiber
JOURNAL Unpublished (1999)
COMMENT Contact: Ben Burr
Biology Department
Brookhaven National Laboratory
Upton, NY 11973, USA
Tel: 516-344-3396
Fax: 516-344-3407
Email: burrb@bnl.bnl.gov
Seq primer: T3 primer.
Location/Qualifiers
1. 646
/organism="Gossypium hirsutum"
/cultivar="Acala Maxxa"
/db_xref="taxon:3635"
/clone_lib="Six-day Cotton fiber"
/tissue_type="immature fiber"
/dev_stage="Six days post anthesis"
/lab_host="XLI-Blue"
/note="Vector: pBluescript II KS+"

BASE COUNT 198 a 141 c 150 g 153 t 4 others
ORIGIN

alignment_scores:
Quality: 111.00 Length: 226
Ratio: 0.941 Gaps: 13
Percent Similarity: 52.212 Percent Identity: 25.221

alignment_block:
US-09-574-735c-2 x AT728644 ..

Align seg 1/1 to: AT728644 from: 1 to: 646

```

6  ArgArgGluArgAspValValGluGluGlnGlyValThrThr..... 20
   ::::::::::: ::::::::::: ::::::::::: :::::::::::
60 AACGAGAGTGCAGAGCAGCTGGAATGGAATGCAACGACGCTTCTC 109
   ::::::::::: ::::::::::: ::::::::::: :::::::::::
21  ....:::.....ThrValysArgArgLysMetGlu..... 29
   ::::::::::: ::::::::::: ::::::::::: :::::::::::
110 ATTATCAAGAGAGAGAAAAGCTGTTGCTTCGAGAAATGCAAGAAATTG 159
   ::::::::::: ::::::::::: ::::::::::: :::::::::::
30  ....:::.....GluValAspLeuValGluSerArgLlelleLeuSer 41
   ::::::::::: ::::::::::: ::::::::::: :::::::::::
160 AGTTAACTTCACCGACATTCAGTTCGGAACCATCGCATCTTTCGAAT 209
   ::::::::::: ::::::::::: ::::::::::: :::::::::::
42  ....:::.....ProCysValGlnAlaThrAsnArgGly.....GlyTl 52
   ::::::::::: ::::::::::: ::::::::::: :::::::::::
210 TCGCTGAACAAACCTATTACTTACTTACTTCCTCGGCTTCTTGAGAGT 259
   ::::::::::: ::::::::::: ::::::::::: :::::::::::
52  eValAlaArgAsnSerAlaGlyAlaSerGluThrSerValValIleVala 69
   ::::::::::: ::::::::::: ::::::::::: :::::::::::
260 GCTTTCGGAGATATGTGTTCCGGT.....:::..... 284
   ::::::::::: ::::::::::: ::::::::::: :::::::::::
69  rGArgArgAspSerProValGluGluGlnCysGlnIleGluGlu 85
   ::::::::::: ::::::::::: ::::::::::: :::::::::::
285  ....:::.....CTCTTCGCGGC 296
   ::::::::::: ::::::::::: ::::::::::: :::::::::::
86  AppSerValSerCysCysSerThrSerGlu.....GluLysSerly 100
   ::::::::::: ::::::::::: ::::::::::: :::::::::::
297 AATTCAATCGGCTTCGTTGTTTCGAGCAACGAGCTGATGATATTCCTCA 346
   ::::::::::: ::::::::::: ::::::::::: :::::::::::
100  sArgArgGlieGluPheValAspLeuGluGlnGlnGlyAspAspArgG 117
   ::::::::::: ::::::::::: ::::::::::: :::::::::::
347 ACATAGCTTGAGATTCGTAGATCTAGAGCGGAAGAGT.....TTTG 387

```

```

117  IuthrGluThrSerTrpIleTyraAspAspLeuAsnLys...SerGluGlu 132
   ::::::::::: ::::::::::: ::::::::::: :::::::::::
388 AACCTAAATCTCA...ACGTGACCAACGCTCAACAATTCAGTAGAGAA 434
   ::::::::::: ::::::::::: ::::::::::: :::::::::::
133  SerMetAsnMetAspSerSerSerValAlaValGluAspValGluSerAr 149
   ::::::::::: ::::::::::: ::::::::::: :::::::::::
435  ACACCTCCCTTAAGCGACATTCGTGAGACTCGGACGAATATCAATCGCC 484
   ::::::::::: ::::::::::: ::::::::::: :::::::::::
149  gArgArgLeuArgLysSerLeuHisGluThrValLys..... 161
   ::::::::::: ::::::::::: ::::::::::: :::::::::::
485  TGAG.....AAAAACCTCCCGCCGTCACAGCAACCGCGGAGATTC 528
   ::::::::::: ::::::::::: ::::::::::: :::::::::::
162  ....:::.....GluAlaGluLeuGluAspPheGlnValAlaGluLysAspLeu 176
   ::::::::::: ::::::::::: ::::::::::: :::::::::::
529  CGTGGCAGCTGAGATGACAGCAATTCCTTCGTCGCGGAAAAAGTAGCAG 578
   ::::::::::: ::::::::::: ::::::::::: :::::::::::
177  ArgAsnLysLeuLeuGluCysSerMetLysTyraAspAspPheGluLys 193
   ::::::::::: ::::::::::: ::::::::::: :::::::::::
579  CAANAAAGATTTCGGAG.....AAGTACNATTATGATATCTCTCA 619
   ::::::::::: ::::::::::: ::::::::::: :::::::::::
193  sAspGluProLeuGluGlyGlyArgTyr 202
   ::::::::::: ::::::::::: ::::::::::: :::::::::::
620  GGATGTGGCTCTC...GACGCTGATAC 644
   ::::::::::: ::::::::::: ::::::::::: :::::::::::
seq_name: gb_est2:BG908519
seq_documentation_block:
LOCUS BG908519 691 bp mRNA EST 05-JUN-2001
DEFINITION Talr1169A02R Talr1 Triticum aestivum cDNA clone Talr1169A02 5',
mRNA sequence.
ACCESSION BG908519
VERSION BG908519.1 GI:14316195
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 691)
AUTHORS Cloutier, S., Dong, G. and Walsh, A.
TITLE Wheat functional genomics - Thatcher Lr1 cDNA library
JOURNAL Unpublished (2001)
COMMENT Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Darke Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
Fax: (204) 983-4604
Email: scloutier@em.agr.ca
was cloned directionally, not all sequences generated with reverse
primer were from the 5' end (same with forward primer and 3' end).
Average inset size is >2.2 kb
Plate: 169 row: A column: 02
Seq primer: M13 Reverse.
Location/Qualifiers
1. 691
/organism="Triticum aestivum"
/cultivar="Thatcher Lr1"
/db_xref="taxon:4565"
/clone_lib="Talr1169A02"
/tissue_type="leaf tissue"
/dev_stage="14 days old"
/lab_host="E. coli XL0LR"
/note="Vector: Lambda ZapII; mass excised in plasmid
vector pBK-CMV (Stratagene).; Site_1: EcoRI; Site_2: XhoI;
mRNA obtained from wheat NIL Thatcher Lr1 24 hours after
inoculation with leaf rust pathogen Puccinia triticina
race BBB carrying the avirulence gene Avr1."
BASE COUNT 141 a 216 c 231 g 103 t
ORIGIN

```

alignment_scores:

Quality: 110.50 Length: 206
Ratio: 1.005 Gaps: 8
Percent Similarity: 53.398 Percent Identity: 23.301

alignment_block:

US-09-574-735C-2 x BG908519 ..

Align seg 1/1 to: BG908519 from: 1 to: 691

```

22 VallysArgArgLysMetGluGluValAspLeuValGluSerArg1 38
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
124 ATGCGCAAGCCCAAGGTCCTCGCGAGGTGCGCTCATGAGAG.....GT 167
38 eileuSerPro.....CysValG 45
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:
168 CGCGCCGCCGCTAGGGTCCGCCACCGCGCAGACCGCTCCGAGGC 217
45 lnaIatHrAsnArgGlyIleValAlaArgAsnSerAlaGlyAlaser 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
218 AGAGGACGCCCGAGGGGGCGGCGTGGCCAAAGACAGGGGAGTACCTG 267
62 GluThrSerValIleValArgArgAspSerPro..... 75
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
268 GAGCTCAGAGTCCGAAAGCTCGAAGAGCTGCCCGCGCGCGCGCGCGC 317
76 .....ValGluGluGlnCysGlnIleGluGluLysAsp 87
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
318 GAGGAGAGAGGCGCGCGCGCGCGAGCGTGGAGCGCCGAGCGCGCGCG 367
87 eRserValSerCysSerThrSerGluLysSerLysArgArgIle 103
   ~:|||||:|||||:|||||:|||||:|||||:|||||:
368 ACGAGGTCTCTTCGGTGAG..... 387
104 GluPheValAspLeuGluLysAsnGlyAspAspArgGluThrGluTh 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
388 AACGTGCTCGAGTCGAGGCCATGGGAGGGGTACACAGGAGACGCC 437
120 rSerTrpIleTyrAspLeuAsnLysSerGluLysSerMetLysMet 137
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
438 CTGC.....ACCTTGATTAGGACTCGGAGACGATAGACACTC 475
137 sPserSerSerValAlaValGluAspValGluSerArgArgArgLeu 153
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
476 CTGATCCACACACAGACCGGACCATGTAATTCACATCGCAGGGTGCA 525
154 LysSerLeuHisGluThrValLys...GluAlaGluLeuGluAspPhe 169
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
526 GCTCCAGCGCGCCATATATATTCATGTTCACAGAGATGATGATTCTT 575
169 eGluValAlaGluLysAspLeuArgAsnLysLeuGluLysSerMetL 186
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
576 CTGCTGCTCGGAGCACCGACAGCAAGCCTTCATTGAC.....A 616
186 ySTyrAsnPheAspPheGluLysAspGluProLeuGlyIleYArgTyr 202
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
617 ACTACAACTTGATCTCTGTGAACGACTCTCTCTC...CCAGGCCGATAC 663
203 GluTrpValLysLeuAsn 208
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
664 GAGTGGGTGAAGCTAAGAC 681

```

seq_name: gb_est2:BG428484

seq_documentation_block:

LOCUS BG428484 1322 bp mRNA EST 14-MAR-2001
DEFINITION 602494996F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4609007 5',
mRNA sequence.

ACCESSION BG428484
VERSION BG428484.1 GI:13334990

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 1322)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LNCM1351 row: 0 column: 24
High quality sequence stop: 230.
Location/Qualifiers

FEATURES

source

```

1. 1322
   /organism="Homo sapiens"
   /db_xref="taxon:9606"
   /clone_image="4609007"
   /clone_lib="NIH_MGC_75"
   /lab_host="DH10B (T1 phage-resistant)"
   /note="Organ: kidney; Vector: pMDR-LIB (Clontech); Site: 1;
   SfiI (ggcgctcgccg); Site: 2; SfiI (ggcattatggc); 5' and
   3' adaptors were used in cloning as follows: 5' adaptor
   sequence: 5'-CACGGCCATATATGCG-3' and 3' adaptor sequence:
   5'-ATTGAGAGCGCGAGCGCGCGGCGGACATG-dt(30)BN-3' (where B = A,
   C, or G and N = A, C, G, or T). Average insert size 1.65
   kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
   by PCR. This library was enriched for full-length clones
   and was constructed by Clontech Laboratories (Palo Alto,
   CA). Note: this is a NIH-MGC Library."

```

BASE COUNT 621 a 232 c 401 g 68 t

ORIGIN

alignment_scores:
Quality: 109.00 Length: 177
Ratio: 1.112 Gaps: 8
Percent Similarity: 55.367 Percent Identity: 25.989

alignment_block:

US-09-574-735C-2 x BG428484 ..

Align seg 1/1 to: BG428484 from: 1 to: 1322

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3 AlayaIArgArgArgGluArgAspValValGluLysAsnGlyValThrTh 19
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901 AGCGGAGAGAGACGACGAGGAGCGCGCGGAGACAA..... 936
19 rThrThValLysArgArgLysMetGluGluGluValAspLeuValGlu 36
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937 AGCGAGACGAGAGAGACAGACAGCGAGAGAGCATGACGAGACAGAG 985
36 eArgGluIleLeuSerProCysValGlnAlaIatHrAsnArgGlyIle 52
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53 ValAlaArgAsnSerAlaGlyAlaserGluThrSerValIleValAr 69
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1005 .....ACGCGAGACAGACGACCAACGAGAC.....AA 1033
69 gArgArgAspSerProValGluGluGlnCysGlnIleGluGluLys 86
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1034 AAGGAGAGAGAGAGAGCGCGCGGAGAGAGAGAGAGAGCAAAAAAACA 1083
86 sPserSerValSerCysSerThrSerGluGluLysSerLysArgArg 102
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seq_name: gb_gss:CNS02PLH

seq_documentation_block:
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DEFINITION Tetradodon nigroviridis genome survey sequence PUC-ori end of clone
            156C05 of library G from Tetradodon nigroviridis, genomic survey
            sequence.
ACCESSION  AL208142.1  GI:7866961
VERSION    AL208142.1  GI:7866961
KEYWORDS   GSS; genome survey sequence.
SOURCE     Tetradodon nigroviridis.
ORGANISM   Tetradodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodon.
REFERENCE  1 (bases 1 to 921)
AUTHORS    Ruest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
            Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetradodon nigroviridis
            Unpublished
            2 (bases 1 to 921)
            Ruest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
            Human gene number estimate provided by genome wide analysis using
            Tetradodon nigroviridis DNA sequence
            Unpublished
            3 (bases 1 to 921)
            Genoscope.
            Direct Submission
            Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
            This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetradodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/tetraodon.
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862 GACAAAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 813
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122 TrpIleTrpAspAspLeuAsnLySserGIUGluserMetAspMet 138
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seq_name: gb_estl:AA655401

seq_documentation_block:
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DEFINITION v10d02.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone
            IMAGE:1211235.5' similar to gb:M58018 MYOSIN HEAVY CHAIN, CARDIAC
            MUSCLE BETA ISOFORM (HUMAN); gb:M76601 Mouse alpha cardiac myosin
            heavy chain mRNA, complete (MOUSE);, mRNA sequence.
ACCESSION  AA655401
VERSION    AA655401.1  GI:2591555
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 653)
            Mairal,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
            The WashU-HM Mouse EST Project
            Unpublished (1996)
            Contact: Maria M/Mouse EST Project
            WashU-HM Mouse EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LNL; contact the

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OM of: US-09-574-735c-2 to: Issued_Patents_NA:* out_format: pfs
Date: Jan 30, 2002 1:20 PM

About: Results were produced by the Gencore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

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-O=/cg2_1/USPTO.spool/US09574735/runat.30012002.101838.814/app-query.fasta.1.270
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-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPEL=0.000
-LOOPEXT=0.000 -OGAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000
-XGAPEXT=0.500 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPEXT=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
-MATRIX=blomum62 -TRANS=human40.cdi -LIST=45 -DOCALLIGN=200
-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTWTF=pfs -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
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Search information block:

Query: US-09-574-735c-2

Query length: 209

Database: Issued_Patents_NA:*

Database sequences: 351203

Database length: 113238999

Search time (sec): 44.180000

score list:

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seq_documentation block:

Sequence 3 Application US/07667276A
Patent No. 5470971
GENERAL INFORMATION:
APPLICANT: Kondo, Keiji
TITLE OF INVENTION: Inocue, Masayori
TITLE OF INVENTION: STRESS-INDUCED PROTEINS, GENES CODING
TITLE OF INVENTION: THEREFOR, TRANSFORMED CELLS OF ORGANISMS, METHODS AND
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weiser & Associates
STREET: 230 S. Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/667,276A
FILING DATE: 11-MAR-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 377,5351P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2017 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
STRAIN: s288C
FEATURE:
NAME/KEY: CDS
LOCATION: 484..1725
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1
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Percent Similarity: 50.990 Percent Identity: 24.257
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US-09-574-735c-2 x US-07-667-276A-3 ..

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101 .....ArgArgIleGluPheValAsp 107
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108 LeuGluGluAsnAsnGlyAsp.....AspArgGluThrGluThrSe 121
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795 AAAAGAACAAACCAAGAAAGAAAGAAATCAAAAGATCTCTGCTGAT 844
138 erSerSerValAlaValGluAspValGluSerArgArgArgLeuArgLys 154
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155 SerLeuHisGluThrValLysGluAlaGluLeuGluAspPheGlnVa 171
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seq documentation block:
; Sequence 5, Application US/08533306A
; Patent No. 5837457
; GENERAL INFORMATION:
; APPLICANT: Liu, Pu
; APPLICANT: Collins, Francis S.
; APPLICANT: Siciliano, Michael J.
; APPLICANT: Claxton, David
; TITLE OF INVENTION: Markers for Detection of Chromosome 16
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI

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; ZIP: 48303
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/533,306A
; FILING DATE: September 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Deann F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 2115-00869COB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 641-1600
; TELEFAX: (810) 641-0270
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2680 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; INDIVIDUAL ISOLATE: Sample 2
; TISSUE TYPE: Acute myelomonocytic leukemia, M4b0
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 16[inv(16)(p13q22)]
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2451
; US-08-533-306A-5

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Ratio: 0.838 Gaps: 13
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alignment_block:
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   :|||: ||||| :|||:
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1093 TCCCTGGCTCG.....GCCCTGAAGAGGCTTGAAGCA 1130
83 uGluGluSerSerValSerCysSerThrSerGlu..... 96
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1131 AGAGAACTCGAGCGACCAACAAATGCTCAAGCCGAAATGGAAGAC 1180
97 .....GluLys 98
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1181 TGTACACTCCAAAGATGACGTGGGCAAGAAAGCTCATGAGCTGAGAG 1230

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99 SerLysArgArgIleGluPheValAspLeuGluGluAsnGlyAspAs 115
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:||||| :||| :|||||
1264 .ATGAAGACGCGAGCTGAAGAGCTGAGGACGAGCTGCAAGCCTCGAGAG 1312
132 Luser.....MetAsnMet..... 136
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1313 ACCGCCAACTGGCGCTGGAAGTCACATGACAGCGCTCAAGGCCAGTTC 1362
137 .....AspSerSerValAlaValGluAspValGluSerArgArg 151
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1363 GAAAGGATCTCCAAAGCCCGGAGCAGCAGATGAGAGAGAGAGAGCA 1412
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168 hePheGluValAlaGluLysAspLeuArg.....Asn 178
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1456 .....GAGCGAAACGACGTCGCCCTGCGACGCTGCGACCAAG 1491
179 LysLeuLeuGluCysSerMetLysTyrAsnPheAspPheGluLysAspG 195
||| :||||| :|||||
1492 AAGAAAGCTGGAAAGGCGACCTGAAA...GACCTGAGCTTCAGCGCGACTC 1538
195 uProLeuGlyGlyArgTyrGluTrpValLys 206
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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-742-923A-5

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seq_documentation_block:
Sequence 5, Application US/08742923A
Patent No. 5869611
GENERAL INFORMATION:
APPLICANT: Liu, Pu
APPLICANT: Collins, Francis S.
APPLICANT: Siciliano, Michael J.
APPLICANT: Claxton, David
TITLE OF INVENTION: Markers for Detection of Chromosome 16
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
STREET: P.O. Box 828
CITY: Bloomfield Hills
STATE: MI
COUNTRY: USA
ZIP: 48303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,923A
-FILING DATE: No. 5869611ember 1, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Deann F.
REGISTRATION NUMBER: 36683
REFERENCE/DOCKET NUMBER: 2115-00869DVC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 641-1600
TELEFAX: (810) 641-0270
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2680 base pairs
type: nucleic acid

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? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA to mRNA
? HYPOTHEICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Homo sapiens
? INDIVIDUAL ISOLATE: Sample 2
? TISSUE TYPE: Acute myelomonocytic leukemia, M4e0
? POSITION IN GENOME: subtype (inv16)
? CHROMOSOME/SEGMENT: 16(inv(16)(p13q22))
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..2451
US-08-742-923A-5

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alignment_scores:
Quality: 100.50 Length: 228
Ratio: 0.838 Caps: 13
Percent Similarity: 52.632 Percent Identity: 25.439

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alignment_block:

US-09-574-735C-2 x US-08-742-923A-5 ..

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961 GGTCCAACTGGAAGAGAGAGAGAGAAATTTGATCAGTTC.....TT 1004
33 uValGluSerArgIleIleLeuSerProCysValGlnAlaThrAsnArg 50
|:||||| :||| :|||
1005 AGCCGAGGAGAAACATCTCTTCCAAATACCGGATGAGGAGCAGAG 1054
50 IyGlyIleValAlaArgAsnSerAlaGlyAlaSerGluThrSerVal 66
:| :||| :|||
1055 CTGAGCAGAGAGCCAGGAG.....AAGCAACCAAGCCCTCG 1092
67 ILeValArgArgArgAspSerProProValGluGluGlnCysGlnIleG 83
:| :||| :|||
1093 TCCCTGGCTCGG.....GCCCTTGAAGAGGCTTGGAGCCCA 1130
83 uGluLysAspSerSerValSerCysSerThrSerGlu..... 96
:| :||| :|||
1131 AAGGAACTCGAGCGGAGCCACCAAAATGCTCAAGCCGAAATGGAAGCC 1180
97 .....GluLys 98
|||||
1181 TGCTACGCTCCAAAGATGACGTGGCGCAACGCTCCATGAGCTGAGAG 1230
99 SerLysArgArgIleGluPheValAspLeuGluGluAsnGlyAspAs 115
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115 pArgGluThrGluThrSerTrpIleTyrAspAspLeuAsnLysSerGluG 132
:||||| :||| :|||||
1264 .ATGAAGACGCGAGCTGAAGAGCTGAGGACGAGCTGCAAGCCTCGAGAG 1312
132 Luser.....MetAsnMet..... 136
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1313 ACCGCCAACTGGCGCTGGAAGTCACATGACAGCGCTCAAGGCCAGTTC 1362
137 .....AspSerSerValAlaValGluAspValGluSerArgArg 151
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1363 GAAAGGATCTCCAAAGCCCGGAGCAGCAGATGAGAGAGAGAGAGCA 1412
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:||||| :||| :|||||
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179 LysLeuLeuGluGlySerMetLysTyrAsnPhaSpheGluLysAspG1 195
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seq_name: /cgn2_6/ptodata/2/lna/5B_COMB.seq:US-08-533-306A-3

seq_documentation_block:
; Sequence 3, Application US/08533306A
; Patent No. 5837457
; GENERAL INFORMATION:
; APPLICANT: Liu, Pu
; APPLICANT: Collins, Francis S.
; APPLICANT: Siciliano, Michael J.
; APPLICANT: Claxton, David
; TITLE OF INVENTION: Markers for Detection of Chromosome 16
; TITLE OF INVENTION: Rearrangements
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: USA
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; - COMPUTER: IBM PC compatible
; - OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/533,306A
; FILING DATE: September 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Deann F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 2115-00869COB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 641-1600
; TELEFAX: (810) 641-0270
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2887 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; INDIVIDUAL ISOLATE: Sample 1
; TISSUE TYPE: Acute myelomonocytic leukemia, M4EO
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 16[inv(16)(p13q22)]
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2658
; US-08-533-306A-3

alignment_scores:
Quality: 100.50 Length: 228
Ratio: 0.838 Gaps: 13
Percent Similarity: 52.632 Percent Identity: 25.439

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33 uValGluSerArgLleIleLeuSerProCysValGluAlaThrAsnArg 50
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50 LgcGlyIleValAlaArgAsnSerAlaGlyAlaSerGluThrSerValAl 66
1262 CTGAGCGAGAACCCAGGAG.....AAGAAACCAAGCCCTG 1299
67 IleValArgArgArgAspSerProProValGluGluGlnGlnIleG1 83
1300 TCCTGGCTCGG.....GCCCTGAAAGAGGCTTGAAGCAAA 1337
83 uGluGluAspSerSerValSerCysCysSerThrSerGlu..... 96
1338 AGAGAACTCGAGCGGACCAACAATGCTCCAAAGCCAAATGGAAGACC 1387
97 .....GluLys 98
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99 SerLysArgArgLleGluPheValAspLeuGluGluAsnAsnGlyAspAs 115
1438 TCCAAGCGGGCCCTGGAG...ACCCAGATGGAGAG..... 1470
115 PargGluThrGluThrSerTrpLleTyrAspAspLeuAsnLysSerGlu 132
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seq_name: /cgn2_6/ptodata/2/lna/5B_COMB.seq:US-08-742-923A-3

seq_documentation_block:
; Sequence 3, Application US/08742923A
; Patent No. 5869611
; GENERAL INFORMATION:
; APPLICANT: Liu, Pu
; APPLICANT: Collins, Francis S.
; APPLICANT: Siciliano, Michael J.
; APPLICANT: Claxton, David
; TITLE OF INVENTION: Markers for Detection of Chromosome 16

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? TITLE OF INVENTION: Rearrangements
? NUMBER OF SEQUENCES: 14
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Hainess, Dickey & Pierce, P.L.C.
? STREET: P.O. Box 828
? CITY: Bloomfield Hills
? STATE: MI
? COUNTRY: USA
? ZIP: 48303
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/742,923A
? FILING DATE: No. 5869611ember 1, 1996
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Smith, Dean F.
? REGISTRATION NUMBER: 36683
? REFERENCE/DOCKET NUMBER: 2115-00869DVC
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (810) 641-1600
? TELEFAX: (810) 641-0270
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 2887 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? MOLECULE TYPE: cDNA to mRNA
? TOPOLOGY: linear
? HYPOTHEICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Homo sapiens
? INDIVIDUAL ISOLATE: Sample 1
? TISSUE TYPE: Acute myelomonocytic leukemia, M4Eo
? POSITION IN GENOME:
? CHROMOSOME/SEGMENT: 16(inv(16)(p13q22))
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..2658
? US-08-742-923A-3

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? Quality: 100.50 Length: 228
? Ratio: 0.838 Gaps: 13
? Percent Similarity: 52.632 Percent Identity: 25.439

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33 uValIuSerArgIleIleLeuSerProCysValGlnAlaThrAsnArg 50
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1212 AGCCGAGGAGAAACATCTCTCCAAATACCGGATGAGAGGACAGAG 1261
50 IyGlyIleValAlaIarGAsnSerAlaGlyAlaSerGluThrSerVal 66
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1262 CTGAGCAGAACACCGAGAG.....AAGGAACCAAGGCCCTG 1299
67 IleValArgArgArgAspSerProValGluGluGlnGlnIleGln 83
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83 uGluIuAspSerSerValSerCysCysSerThrSerGlu..... 96
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97 .....GluIys 98
1388 TGGTCAGCTCCAAGATGACGTGGGCAAGACGTCATGACGTGGAGAG 1437
99 SerIysArgArgIleGluPheValAspLeuGluGluAsnArgIlyAsp 115
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115 pArgGluThrGluThrSerThrPleTyraSpAspLeuAsnIysSerGlu 132
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132 IuSer.....MetAsnMet..... 136
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137 .....AspSerSerSerValAlaValAlaGluAspValGluSerArgAr 151
1570 GAAAGGATCTTCAAGCCCGGAGCAGAGATGAGAGAGAGAGAGCA 1619
151 gluArgIysSerLeuHisGluThrValIysGluAlaGluLeuGluAsp 168
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1620 ACTGCAGACAGACCTTCACAGAG.....TATGAGACGGAACCTGGAAG 1662
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1663 .....GAGCGAAACGAAACGTGCCCTGACAGCTCAGACGAAG 1698
179 LysLeuLeuGluCysSerMetIysTyraSnPheAspPheGluIysAsp 195
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seq_name: /cgn2_6/ptodata/2/1na/6A_COMB.seq:US-09-214-564A-5
seq_documentation_block:
? Sequence 5, Application US/09214564A
? Patent No. 6150515
? GENERAL INFORMATION:
? APPLICANT: Sharp, Phillip A.
? TITLE OF INVENTION: TAT-SF: Cofactor For Stimulation Of Transcriptional
? FILE REFERENCE: M0656/7042 Elongation By HIV-1 TAT
? CURRENT APPLICATION NUMBER: US/09/214,564A
? PRIOR FILING DATE: 1999-08-18
? PRIOR APPLICATION NUMBER: US 60/021,218
? PRIOR FILING DATE: 1996-07-03
? PRIOR APPLICATION NUMBER: US 60/033,152
? PRIOR FILING DATE: 1996-12-13
? PRIOR APPLICATION NUMBER: PCT/US97/11713
? NUMBER OF SEQ ID NOS: 5
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 5
? LENGTH: 2672
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 58..2319
? US-09-214-564A-5

alignment_scores:
? Quality: 100.00 Length: 211
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Ratio: 0.971 Gaps: 12
Percent Similarity: 48.815 Percent Identity: 26.066

alignment block:

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Align seg 1/1 to: US-09-214-564A-5 from: 1 to: 2672

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44 LglAlaThrAsnArgIleGlyIleValAlaArgAsnSerAlaGlyAla 61
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61 ergIuThrSerValIleValAlaArgArgAspSerProValGlu 77
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1388 CTGAAACCAATGCT.....AAGGAAAGTACCCCGAAGAAAGAG 1425
78 GluGluGlnSerGlnIleGluGluGluAspSerSerValSerCys..... 91
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1426 GCTGAAGAGAGCTCCCTCGAAGAAAGATCTGAGAGAGGCTCCCGCAAG 1475
92 .....CysSerThrSerGlu..... 96
1476 AGGGTTTGAAGCAGCTGCTCCCAAGAGAGTCTGAGAGAGCAATCCCG 1525
97 .....GluysSerLysArgArgIle 103
1526 TAAGAGATCTGAAGAGAGATAGTCTAAGAAAGAGTCTAAGAAAGACACA 1575
104 GluPheValAspLeuGluGluAsnArgIleValAspArgGluThr 120
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1576 CTCGAAATATGATTTGTGAAG..AATGCCCTTGCAGAGAGATCTGAA.. 1620
120 rSerTrpIleTyrAspAspLeuAsnLys..... 129
1621 .....GATGACCTCAACAGAGAGTCTGAGAGAGGCTGGCC 1657
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184 SerMetLysTyrAsnPheAspPheGluLysAsp 194
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seq documentation block:
; Sequence 1, Application US/09214564A
; Patent No. 6150515
; GENERAL INFORMATION:
; APPLICANT: Sharp, Phillip A.
; APPLICANT: Zhou, Qiang
; TITLE OF INVENTION: RAT-SF: Cofactor For Stimulation Of Transcriptional
; TITLE OF INVENTION: Elongation By HIV-1 TAT
; FILE REFERENCE: M0656/7042
; CURRENT APPLICATION NUMBER: US/09/214,564A
; CURRENT FILING DATE: 1999-08-18

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; PRIOR APPLICATION NUMBER: US 60/021,218
; PRIOR FILING DATE: 1996-07-03
; PRIOR APPLICATION NUMBER: US 60/033,152
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: PCT/US97/11713
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2815
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 110..2371
; NAME/KEY: unsure
; LOCATION: 46..46
; OTHER INFORMATION: n = a, c, g or t
; NAME/KEY: unsure
; LOCATION: 2731..2731
; OTHER INFORMATION: n = a, c, g or t
; US-09-214-564A-1

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alignment scores: Quality: 100.00 Length: 211
Ratio: 0.971 Gaps: 12
Percent Similarity: 48.815 Percent Identity: 26.066

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1400 .GAAAGACAGAGATGAGGGA.....GAATTGAGAGAGTCTT 1439
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61 ergIuThrSerValIleValAlaArgArgAspSerProValGlu 77
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1528 AGGGTTTGAAGCAGCTGCTCCCAAGAGAGTCTGAGAGAGCAATCCCG 1577
97 .....GluysSerLysArgArgIle 103
1578 TAAGAGATCTGAAGAGATAGTCTAAGAAAGAGTCTAAGAAAGACACA 1627
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152 ..:::|||||:||||| 111
153 |||:|||||:||||| 111
1810 TGCTTCAGAGAAAGATTGGACGAGGAAGTTCTGAAAGAGCTTCATG 1555
167 spPhepGhG1aValaLagLylusAspLeuArGAsnLysLeuLeuGluCys 1833
1860 AA.....AAGTCTTCGACAAAGAGTTAGAAAGAAATGACTCTGAA... 1906
184 SerMetLysTYrAsnPhaSpheGluLysAsp 194
1901 .....AAGTCGAATTGGAAATGAAATGAC 1921

seq_name: /cgn2_6/ptodata/2/1na/5A_COMB.seq:US-08-374-077C-1

seq_documentation_block:
Sequence 1, Application US/08374077C
Patent No. 6027912
GENERAL INFORMATION:
APPLICANT: Hall, Linda M.
APPLICANT: Ren, Dejian
APPLICANT: Zheng, Wei
APPLICANT: Dubaid, Manuel Marcel Paul
TITLE OF INVENTION: Genes Encoding an Invertebrate Alpha1
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DONALD, SWECKER & MATHIS, LLP
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,077C
FILING DATE: 19-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm M.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 022650-264
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8075 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 157..7704
US-08-374-077C-1

alignment_scores:
Quality: 98.00 Length: 208
Ratio: 0.891 Gaps: 8
Percent Similarity: 52.885 Percent Identity: 17.788

alignment_block:
US-09-574-735C-2 x US-08-374-077C-1 ..
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1117 GTAGCGCAATTGGCGCAGACGCAAGAACAGGCCAGGACAAATTCGT 1166
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1167 CGCCGACTGCAGAGCTTCAAGCGATCCGCCGACAGATCCCAGTAGAGCG 1216
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31 alaAspLeuValGlnSerArgIleIleLeuSerProCysValGIgnLThr 47
      |||||||
1217 TCCGCAATTCACAGAT.....TGCCTCGCGCGGCAC 1248
      |||||||
48 AsnArgIgLylIleValAlaIleArgAsnSerAlaGlyAlaSerGluThrSe 64
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1249 AACGACTCA.....CTCGAAGACGTTGGCGAGTGAGCACAAACC 1289
      |||||||
64 rValValIleValArgArg.....ArgAspSerProProValGIguIgu 79
      :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
1290 CGAGCGTTGCTGTGAAGAAGAACTCAAGGAATCGTCTCGATCAGAAAGA 1339
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79 IpcyGlnIleGIguIguLysPserSerValSerCysCysSerThrSer 95
      |||||||
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96 GIUGlUdYsSerLysArgArgIleGIuPheValAspLeuGIguLuanas 112
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1363 .....GACGACGAGACGAGNA 1379
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112 nglYaspAspArgGlUthrGluThrSerTrpIleTyraSpAspLeuAsnL 129
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1380 CCGCGAC.....TACGGTGATTCGATC 1402
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129 ySserGIguLysSerMetAsn.....MetAspSerSerGeyAla 142
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1403 GGGAGGATCAAGACTGAGACAGCAGAGAGCCCCGAGGCGCACCATTCGAC 1452
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143 ValGIuLysPValGlnSerArgArgArgLeuArgLysSerLeuHisGIuTh 159
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176 euArgAsnLysLeuLeuGIguLysSerMetLysTYraSnPhesPheGIu 192
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1591 CTATTGATAATTTCGTGGCGGCT 1614
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seq_name:/cgn2_6/p/odata/2/lna/bb_COMB.seq;US-08-895-590-1
seq_documentation_block:
? Sequence 1, Application US/08895590
? Patent No. 6207410
? GENERAL INFORMATION:
? APPLICANT: Hall, Linda M.
? APPLICANT: Ren, Dejian
? APPLICANT: Zheng, Wei
? APPLICANT: Dubaiid, Manuel Marcel Paul
? TITLE OF INVENTION: Genes Encoding an Insect Calcium Channel
? NUMBER OF SEQUENCES: 101
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
? STREET: 699 Prince Street
? CITY: Alexandria
? STATE: VA
? COUNTRY: USA
? ZIP: 22314-3187
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible

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[illegible]


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80 CysGlnIleGluGluGluAspSerSerValSerCysSerThrSerg1 96
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96 uGluSerSerIysArgArgIleGluPheValAspLeuGluGluAsnAng 113
   ::::: ::::: ::::: ::::: ::::: :::::
1534 AGAGCTCCAGGAGAGAGCTAAAGCTTACCTACCTCAGGAAAAAT 1579
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113 LysAspAspArgIuThrGluThrSerThrPleItyrAspAspLeuAsnIys 129
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1580 ..... TTGAGTGAAGTCACTCAAGTGAAGAGACTTGGAATAA 1618
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130 SerGluGluSerMetAsnMetAspSerSerValAlaValGluAspVa 146
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146 IGLuSerArgArgArgLeuArgIysSerLeuHISGluThrVal..LysG 162
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1669 CTCT..... GTTCAGAGAGAGATGCAAGAACTGTAAATAAGT 1706
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   ::::: ::::: ::::: :::::
1707 TACACCAAAAGAGAGAACGTTTAACATGCTCTCTGACTTGAGAGAG 1756
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176 LeuArgAsnIysLeuLeuGluCysSerMetIysTyrAsnPheAspPheG1 192
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seq documentation block:
; Sequence 67, Application US/08235836C
; Patent No. 6248562
; GENERAL INFORMATION:
; APPLICANT: Dunn, John J.
; APPLICANT: Luft, Benjamin J.
; TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
; TITLE OF INVENTION: Borrelia Polypeptides and Uses Therefor
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brookhaven National Laboratory
; STREET:
; CITY: Upton
; STATE: NY
; COUNTRY: USA
; ZIP: 11973
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,836C
; FILING DATE: 29-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,191
; FILING DATE: 01-11-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Bogosian, Margaret C.
; REGISTRATION NUMBER: 25,324
; REFERENCE/DOCKET NUMBER: BNL93-28A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 282-7338
; TELEFAX: (516) 282-3729
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2081 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2081
; US-08-235-836C-67

alignment_scores:
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  Ratio: 0.889 Gaps: 7
  Percent Similarity: 49.091 Percent Identity: 21.364

alignment_block:
US-09-574-735C-2 x US-08-235-836C-67 ..
Align seg 1/1 to: US-08-235-836C-67 from: 1 to: 2081

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22 LysArgArgIysMetGluGluGluValAspLeuValGluSerArgIle 39
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39 IeLeuSerProCysValGluAlaThrAsnArgGlyIleValAlaArg 55
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1012 .....
56 AsnSerAlaGlyAlaSerGluThrSerValValIleValArgArgArg 72
   :::::
1015 AATTGGCAAAACCTGGGATGTAAGT.....AAG 1041
   :::::
72 PserProProValGluGluGluCysGlnIleGluGlu.....GluAsp 87
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1042 TCTCTTAAGTGTATGATTAAGCAGCTACCAAAATAAGAGCTTACAGAGACT 1090
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87 erSerValSerCysSerThrSerGluGluLysSerIysArgArgIle 103
   :::::
1091 TGCAGAGACACTTAAGAAACTGACGTGAAATTCAAAAGAGCAATTT 1140
   :::::
104 GluPheValAspLeuGluGluAsnAsnGlyAspAspArgGluThrGlu 120
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1141 GAA.....AAGCAAAATTGAAAT 1157
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120 rSerThrPleItyrAspAspLeuAsnIysSerGluGluSerMetAsnMet 137
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1158 CAAAAAAGTGATGAGAGAACTTTTAAAAAGTAAGATCTTAAAGCATTAAG 1207
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137 spSerSerSerValAlaValGluAspValGluSerArgArgArgIle 153
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154 LysSerLeuHISGluThrValIysGlu.....AlaG1 164
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164 uLeu.....G 166
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166 LysAspPhePheGluValAlaGluLysAspLeuArg..... 177
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178 AsnIysLeuLeuGluCysSerMetIysTyrAsnPheAspPheGluIysAs 194
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194 pGluProLeu 197

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APPLICANT: Jon D. Kratochvil
APPLICANT: Eric Russell
APPLICANT: Stephen D. Stroupe
TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the Urinary
FILE REFERENCE: 6180, US, 01
CURRENT APPLICATION NUMBER: US/09/153, 804
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 1724
TYPE: DNA
ORGANISM: Homo sapiens
US-09-153-804-8

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  Percent Similarity: 50.235      Percent Identity: 22.535

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40 userProcysValGlnAlaIleThrAsnArgGlyIleValAlaArgAsn 57
751 ..... 751
57 eraIaGlyAlaSerGluThrSerValValle.....ValArg 69
||||| ||||||| ||||||| ||||||| |||||||
752 .....TCGGACACATCTGTGTCTGTCTGTCCATGACACAGCCGC 790
70 ArgArgAspSerProValGluGluGlnCysGlnIleGluGluGluAs 86
||||| ||||||| ||||||| ||||||| |||||||
791 TCCCTGGACATGAGACATCATTCATGCTGAGTCAAGGCACAGTACGAGA 840
86 pSerSerValSerCysSerThrSerGluGluGluSerLysArgArgI 103
||||| ||||||| ||||||| ||||||| |||||||
841 T.....ATTGCCAACCGCAGCCGGCTGAGCTGAGACATGTACAGAGA 884
103 IeGluPheValAspLeuGluGlu.....AsnAsnGlyAspAsp... 115
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885 TCAGATGATGAGAGCTGAGAGCTGCTGGAGAACGACGGGATGACCTG 934
116 ArgGluThrGluThrSerTrpIleTyrAspAspLeuAsnLysSerGlu 132
||||| ||||||| ||||||| ||||||| |||||||
935 CGGCGCACAAGACTGAG.....ATCTCAGATGTAACCGGAACATCAG 978
132 userMetAspMetAsp.....Sersers 140
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979 CCGGCTCCAGGCTGAGATGAGGCTCAAGGCCAGAGGCTTCCCTGG 1028
140 eraValAlaValAlaGluAspValGluSerArgArgLeuArgLysSer 156
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1029 AGGCGCGCATTCGATGCGCAGCAGCGTGGAGAGCTG..... 1066
157 HisGluThrValLysGluAla.....GluLeuGluAspPh 168
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1067 .....GCCATTAGAGATGCCAACGCCAAGTTGTCCAGCTGGAGCGC 1110
168 ephGluValAlaGluLysAspLeuArgAsnLysLeuGlu..... 182
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1111 CCTTCACGCGGCCAAGCAGACATGCGCCGCGACCTCGTGTAGTACAGG 1160
183 .....CysSerMetLysTyrAsnPheAspPheGlu..... 192
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Sequence 2, Application US/08973462B
Patent No. 6131270
GENERAL INFORMATION:
APPLICANT: DROULHE, PIERRE
APPLICANT: DAUBERSIES, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
FILE REFERENCE: 0660-0125-0 PCT
CURRENT APPLICATION NUMBER: US/08/973,462B
EARLIER FILING DATE: 1998-02-06
EARLIER APPLICATION NUMBER: PCT/FR96/00894
EARLIER FILING DATE: 1996-06-12
EARLIER APPLICATION NUMBER: FR 95/07007
EARLIER FILING DATE: 1995-06-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 5361
TYPE: DNA
ORGANISM: P. falciparum
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(5361)
US-08-973-462-2

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  Percent Similarity: 51.659      Percent Identity: 24.171

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alignment_block:

US-09-574-735c-2 x US-08-973-462-2 ..

Align seg 1/1 to: US-08-973-462-2 from: 1 to: 5361

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13 uGluAsnGlyValThrThrThrValLys.....ArgArgLysM 27
||||| ||||||| ||||||| ||||||| |||||||
3624 AGACAATGATATGATGATGAAAGTGTGAGAAAGTTTGAATGAAAAATA 3673
27 etGluGluGluVal.....AspLeuValGluSerArgIleIleSer 41
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3674 TGGAGAGGAGTTTAAGACAGATGCTTTGAAATAATGACATTACTAGC 3723
42 ProcysValGlnAlaThrAsnArgGlyIleValAlaIleArgAsn..... 56
||||| ||||||| ||||||| ||||||| |||||||
3724 AAACATTATTAAGAACTCAAGATTAATGAAGTAGAACAGATTAAAT 3773
57 .....SerAlaGlyAlaSerGluThr 64
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3774 AAAAGATATGAAAAATTAAAGAAATTAGAAAAAGCTTATTCAGAGATT 3823
64 eraValValIleValArgArgArgAsp.....SerProProValGlu 77
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3824 CTAAGAAATTAATAGATCAAAAGATGATACATTAGAAAAATTATTGAA 3873
78 GluGlnCysGlnIleGluGluGlu.....AspSerSerValSerCys 93
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3874 GAGGAACATGATTAATACGACAGCTTGATGAAGTTTAAATTAAGA 3923
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Db 55469 GAGGATTACATCAAGAGACTAGAGAGATTGGATTGTAATGTGCAAGAGAGAT 55410
QY 241 GCCCTCAATTGATTGAGAGGCTG 266
Db 55409 GCCCTCAATTGATTGAGAGGCTG 55384

RESULT 7
LOCUS CRCYCD 1699 bp mRNA PLN 19-JUN-1997
DEFINITION C.rubrum mRNA for cyclin-D like protein.
ACCESSION Y10162
VERSION Y10162.1 GI:1770189
KEYWORDS cyclin gene; cyclin-D like protein.
SOURCE red goosefoot.
ORGANISM Chenopodium rubrum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Caryophyllales; Chenopodiaceae; Chenopodium.
1 (bases 1 to 1699)
REFERENCE 1
Renz,A.
TITLE Direct Submission
JOURNAL Submitted (18-DEC-1996) A. Renz, Lehrstuhl fuer
Pflanzenphysiologie, Universitaet Bayreuth, Universitaetsstr. 30,
95447 Bayreuth, FRG
2 (bases 1 to 1699)
Renz,A., Fountein,M. and Beck,E.
Nucleotide sequence of a cDNA encoding a D-type cyclin from a
photoautotrophic cell suspension culture of Chenopodium rubrum L
Plant Physiol. In press
FEATURES
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1. 1699
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DKAFSLTDHVEKRMKCVETIMHDLMSRSNGALASTSVSPISGIVDASCLSYK
SDSTSTPGSCNSAHSSPASPAPRRKRLDRTSIS"
BASE COUNT 554 a 283 c 308 g 552 t 2 others
ORIGIN
Query Match 27.9%; Score 258.2; DB 8; Length 1699;
Best Local Similarity 64.0%; Pred. No. 2,5e-54;
Matches 440; Conservative 0; Mismatches 238; Indels 9; Gaps 3;
QY 123 GAGAGTGAGAGATTATCATGAGATGTGAGAGAGAGACGATTTGCCAGTGA 182
Db 603 GCGAAATCATGAGTGTGCTCTCTGTTGACAAAGAAACAAATTTCTGCGCTC 662
QY 183 TGATTACATCAAGAGATTGAGAGATTGGATTGAATGTGCAAGAGAGATGC 242

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Db 722 -TTGATTGATTCAATCAAGATTCACATCCACATCAATTTGGGCCACTTGTCTTATCT 779
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Db 780 ATCTGTAACCTTGTGATCGCTTCTTCTGCTTATGATTAAC--TGCAACCTTG 836
QY 363 GATATTGACAGTTGTGCTGCTGCTTTTATCATTTGAGCAACCAATGAGAACTGA 422
Db 837 GATGATGCAATTCCTGCTGCTGCTTCTTATTCATGCTGCAAGGTGATGAACCTGA 896
QY 423 AGTTCCAAATGATTGATGATTCAGTTGAGAGATTCCTGATTTGTGTTGAGGCTTAATC 482
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QY 483 AGTCCAAAGATGAGCTTTTGTGTTGAACAATGGAATGAGATTTGAGACCAATAC 542
Db 957 AATCCAAAGATGAGCTTTTGTGTTGAGACCTTTGAGTGAAGTGAAGTGAAGTGAAGTGA 1016
QY 543 TCCATGCTCATATGATGATTTCTGAGAAAGATGATGAATGATGATCAAGACCATC 602
Db 1017 ACCATTTCTTTATGATGATTTCTTATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1073
QY 603 CAACACATGATATCTAGATCATTAAGATGAGCAGACACCAACCAAGATTAAGCTT 662
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Db 1134 GATGAGATTTCAGACCTTCAAAATATACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1193
QY 723 GCAGAGTACACTTTCAGACCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 782
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QY 783 GAGAGTGAAGAGATGAGGGAATGAT 809
Db 1254 GAGATTGATGAATGTGTTGAGATTAAT 1280

RESULT 8
LOCUS A85077 1846 bp DNA PAT 21-JAN-2000
DEFINITION Sequence 21 from Patent WO9842851.
ACCESSION A85077
VERSION A85077.1 GI:673818
KEYWORDS
SOURCE
ORGANISM
Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PAC
Clade: Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1846)
REFERENCE 1
Murray,J.A.
PLANTS WITH MODIFIED GROWTH
Patent: WO 9842851-A 21.01.OCT-1998;
JOURNAL MURRAY JAMES AUGUSTUS HENRY (GB); UNIV CAMBRIDGE TECH (GB)
FEATURES
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1. 1846
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Best Local Similarity 59.8%; Pred. No. 4.4e-38;
Matches 364; Conservative 0; Mismatches 236; Indels 9; Gaps 2;

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